



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:10 AM UTC

PDB ID : 6I2R / pdb_00006i2r
Title : Crystal structure of the SucA domain of Mycobacterium smegmatis KGD (alpha-ketoglutarate decarboxylase), mutant R802A, in complex with GarA
Authors : Wagner, T.; Bellinzoni, M.; Alzari, P.M.
Deposited on : 2018-11-01
Resolution : 2.20 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

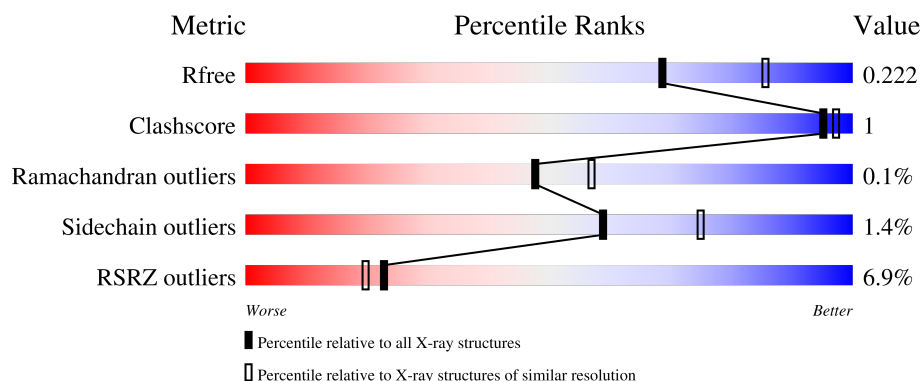
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	868	 6% 90% 5% 5%
1	C	868	 7% 91% 5%
2	B	115	 3% 77% 18%
2	D	115	 14% 72% 8% 20%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14687 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 Multifunctional 2-oxoglutarate metabolism enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	824	Total	C	N	O	S	0	2	0
			6419	4051	1130	1214	24			
1	C	822	Total	C	N	O	S	0	1	0
			6343	4008	1113	1198	24			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	360	GLY	-	expression tag	UNP A0R2B1
A	802	ALA	ARG	engineered mutation	UNP A0R2B1
C	360	GLY	-	expression tag	UNP A0R2B1
C	802	ALA	ARG	engineered mutation	UNP A0R2B1

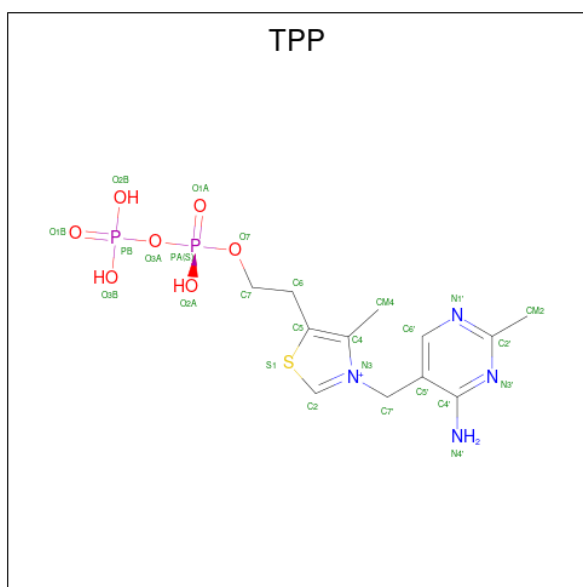
- Molecule 2 is a protein called Glycogen accumulation regulator GarA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	94	Total	C	N	O	0	0	0
			716	449	131	136			
2	D	92	Total	C	N	O	0	0	0
			699	440	126	133			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	44	GLY	-	expression tag	UNP A0QYG2
D	44	GLY	-	expression tag	UNP A0QYG2

- Molecule 3 is THIAMINE DIPHOSPHATE (CCD ID: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
3	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	C	1	Total	Ca	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	240	Total	O	0	0
			240	240		

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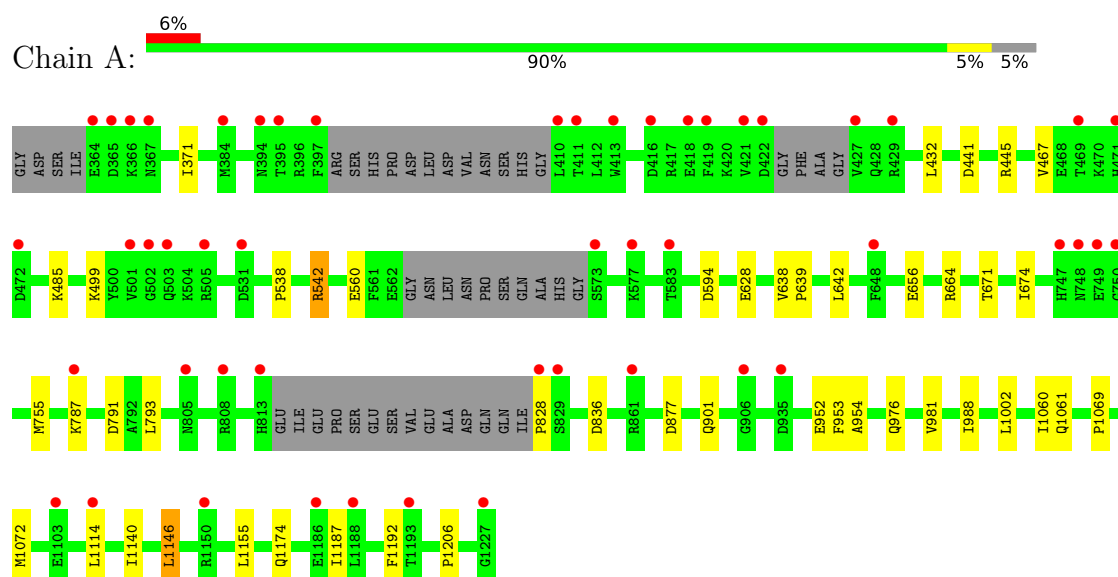
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	13	Total 13	O 13	0	0
6	C	194	Total 194	O 194	0	0
6	D	7	Total 7	O 7	0	0

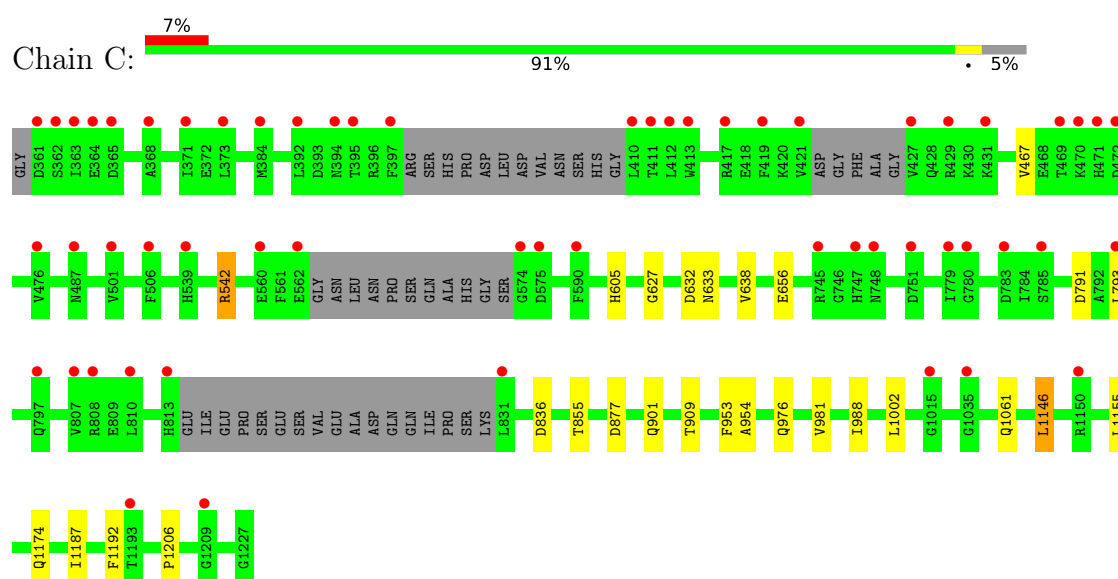
3 Residue-property plots [i](#)

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.

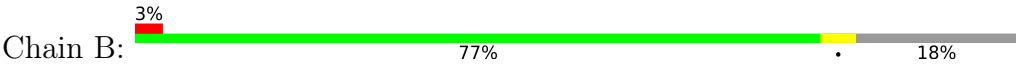
- Molecule 1: Multifunctional 2-oxoglutarate metabolism enzyme



- Molecule 1: Multifunctional 2-oxoglutarate metabolism enzyme



- Molecule 2: Glycogen accumulation regulator GarA



● Molecule 2: Glycogen accumulation regulator GarA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.75Å 143.15Å 167.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.15 – 2.20 48.15 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.6 (48.15-2.20) 96.6 (48.15-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.195 , 0.219 0.198 , 0.222	Depositor DCC
R_{free} test set	5714 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14687	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CA, TPP

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	0.86	0/6554	1.18	7/8875 (0.1%)
1	C	0.86	0/6473	1.19	8/8777 (0.1%)
2	B	0.76	0/728	1.01	0/987
2	D	0.72	0/711	0.98	0/965
All	All	0.85	0/14466	1.17	15/19604 (0.1%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	594	ASP	CA-CB-CG	6.44	119.04	112.60
1	C	953	PHE	CA-CB-CG	6.37	120.17	113.80
1	A	836	ASP	CA-CB-CG	6.03	118.63	112.60
1	C	836	ASP	CA-CB-CG	5.77	118.37	112.60
1	A	638	VAL	N-CA-C	5.63	114.08	107.77
1	C	877	ASP	CA-CB-CG	5.56	118.16	112.60
1	A	953	PHE	CA-CB-CG	5.56	119.36	113.80
1	A	877	ASP	CA-CB-CG	5.47	118.07	112.60
1	C	791	ASP	CA-CB-CG	5.46	118.06	112.60
1	C	632	ASP	CA-CB-CG	5.31	117.91	112.60
1	A	952	GLU	N-CA-C	-5.30	105.94	112.72
1	C	638	VAL	N-CA-C	5.22	113.61	107.77
1	A	791	ASP	CA-CB-CG	5.05	117.65	112.60
1	C	627	GLY	CA-C-N	5.01	127.30	120.54
1	C	627	GLY	C-N-CA	5.01	127.30	120.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6419	0	6260	20	0
1	C	6343	0	6132	9	0
2	B	716	0	705	2	0
2	D	699	0	684	4	0
3	A	26	0	16	1	0
3	C	26	0	16	1	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	240	0	0	1	0
6	B	13	0	0	0	0
6	C	194	0	0	0	0
6	D	7	0	0	0	0
All	All	14687	0	13813	34	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 1.

All (34) 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:828:PRO:HB3	1:A:1060:ILE:HD11	1.59	0.83
1:A:441:ASP:HA	1:A:445:ARG:CD	2.23	0.68
1:A:441:ASP:HA	1:A:445:ARG:HD3	1.76	0.66
1:A:642:LEU:HD22	1:A:674:ILE:HB	1.81	0.63
2:D:61:ARG:HB2	2:D:142:ARG:HB2	1.86	0.56
1:A:656:GLU:HB3	1:A:954:ALA:HB2	1.88	0.55
1:A:1002:LEU:HB3	1:A:1061:GLN:HB2	1.91	0.53
1:A:828:PRO:CB	1:A:1060:ILE:HD11	2.35	0.53
1:A:542:ARG:HH11	1:A:542:ARG:HG3	1.75	0.52
1:C:656:GLU:HB3	1:C:954:ALA:HB2	1.90	0.52
1:C:1002:LEU:HB3	1:C:1061:GLN:HB2	1.94	0.48
1:A:441:ASP:HA	1:A:445:ARG:HD2	1.92	0.48
1:C:542:ARG:HH11	1:C:542:ARG:HG3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1146:LEU:HD22	1:C:1187:ILE:HD11	1.96	0.48
1:A:639:PRO:HB2	1:A:671:THR:HG23	1.96	0.47
1:A:981:VAL:HG22	1:A:988:ILE:HD11	1.97	0.46
1:A:628:GLU:HG2	1:A:664:ARG:O	2.15	0.46
1:C:981:VAL:HG22	1:C:988:ILE:HD11	1.97	0.45
1:A:1155:LEU:HD11	1:A:1192:PHE:CZ	2.52	0.45
1:C:1155:LEU:HD11	1:C:1192:PHE:CZ	2.53	0.44
1:A:1146:LEU:HD12	1:A:1187:ILE:HD11	2.00	0.43
1:C:1174:GLN:OE1	1:C:1206:PRO:HA	2.19	0.43
2:D:119:TYR:HB2	2:D:137:GLN:HB3	2.02	0.42
1:A:755:MET:HE1	1:C:909:THR:HG21	2.01	0.42
1:A:538:PRO:HD2	6:A:2198:HOH:O	2.20	0.42
1:A:1174:GLN:OE1	1:A:1206:PRO:HA	2.20	0.42
1:A:1114:LEU:HD21	1:A:1140:ILE:HD11	2.02	0.42
2:D:75:THR:HG22	2:D:101:ARG:HG2	2.01	0.41
1:A:1069:PRO:CB	1:A:1072:MET:HB3	2.51	0.41
2:D:97:HIS:CD2	2:D:138:ILE:HG23	2.55	0.41
3:A:2001:TPP:H6'	1:C:901:GLN:OE1	2.20	0.41
1:A:901:GLN:OE1	3:C:2001:TPP:H6'	2.21	0.40
2:B:97:HIS:CD2	2:B:138:ILE:HG23	2.57	0.40
2:B:119:TYR:HB2	2:B:137: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	816/868 (94%)	798 (98%)	18 (2%)	0	100	100
1	C	813/868 (94%)	795 (98%)	17 (2%)	1 (0%)	48	57
2	B	92/115 (80%)	88 (96%)	4 (4%)	0	100	100
2	D	90/115 (78%)	87 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1811/1966 (92%)	1768 (98%)	42 (2%)	1 (0%)	48 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	605	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	666/725 (92%)	655 (98%)	11 (2%)	53 69
1	C	647/725 (89%)	640 (99%)	7 (1%)	65 79
2	B	77/93 (83%)	76 (99%)	1 (1%)	61 76
2	D	75/93 (81%)	74 (99%)	1 (1%)	61 76
All	All	1465/1636 (90%)	1445 (99%)	20 (1%)	59 75

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	371	ILE
1	A	432	LEU
1	A	467	VAL
1	A	485	LYS
1	A	499	LYS
1	A	542	ARG
1	A	560	GLU
1	A	787	LYS
1	A	793	LEU
1	A	976	GLN
1	A	1146	LEU
2	B	103	GLU
1	C	467	VAL
1	C	542	ARG

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Mol	Chain	Res	Type
1	C	633	ASN
1	C	793	LEU
1	C	855	THR
1	C	976	GLN
1	C	1146	LEU
2	D	56	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	539	HIS
1	A	556	GLN
1	A	679	GLN
1	A	797	GLN
1	A	799	GLN
1	A	912	HIS
1	A	1001	GLN
1	C	556	GLN
1	C	679	GLN
1	C	799	GLN
1	C	1001	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	TPP	C	2001	4	26,27,27	0.53	0	38,40,40	0.58	0
3	TPP	A	2001	4	26,27,27	0.40	0	38,40,40	0.63	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	TPP	C	2001	4	-	0/17/17/17	0/2/2/2
3	TPP	A	2001	4	-	2/17/17/17	0/2/2/2

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	A	2001	TPP	C7-O7-PA-O1A
3	A	2001	TPP	PA-O3A-PB-O1B

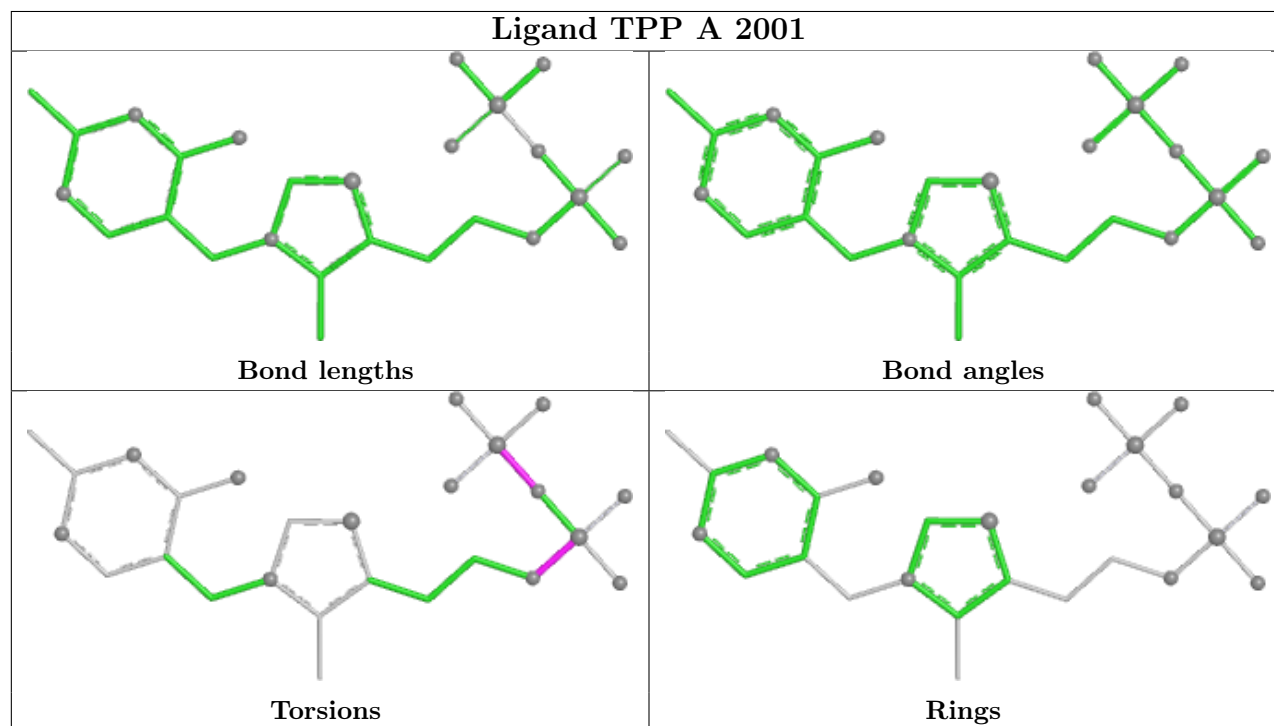
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2001	TPP	1	0
3	A	2001	TPP	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	824/868 (94%)	0.29	50 (6%)	27	24	15, 29, 58, 91	2 (0%)
1	C	822/868 (94%)	0.39	57 (6%)	23	20	17, 31, 61, 89	1 (0%)
2	B	94/115 (81%)	0.39	3 (3%)	50	47	24, 36, 60, 70	0
2	D	92/115 (80%)	1.32	16 (17%)	4	3	36, 57, 83, 100	0
All	All	1832/1966 (93%)	0.39	126 (6%)	23	20	15, 31, 63, 100	3 (0%)

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	562	GLU	6.0
1	C	421	VAL	5.9
1	C	394	ASN	5.9
2	D	147	THR	5.6
1	C	368	ALA	5.5
1	A	828	PRO	5.5
1	C	363	ILE	5.5
1	A	394	ASN	5.4
1	A	422	ASP	5.2
1	A	397	PHE	5.2
1	A	502	GLY	5.2
1	A	364	GLU	5.0
1	A	421	VAL	4.9
1	A	427	VAL	4.8
1	A	747	HIS	4.8
1	C	831	LEU	4.8
1	C	411	THR	4.6
1	C	410	LEU	4.6
1	C	747	HIS	4.6
1	C	813	HIS	4.6
1	A	813	HIS	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	805	ASN	4.3
1	A	472	ASP	4.3
1	C	427	VAL	4.2
1	C	785	SER	4.2
1	A	748	ASN	4.1
1	A	573	SER	4.0
1	A	413	TRP	3.9
1	A	365	ASP	3.8
1	C	364	GLU	3.8
2	B	147	THR	3.8
1	A	906	GLY	3.6
1	C	361	ASP	3.6
1	C	501	VAL	3.6
1	C	1193	THR	3.6
1	A	750	GLY	3.5
1	A	501	VAL	3.5
1	A	861	ARG	3.4
1	C	1035	GLY	3.4
1	C	397	PHE	3.4
2	B	54	SER	3.3
1	A	787	LYS	3.3
2	D	56	LEU	3.3
1	C	395	THR	3.3
1	C	780	GLY	3.1
1	A	411	THR	3.1
1	A	410	LEU	3.1
2	D	138	ILE	3.0
1	C	365	ASP	3.0
1	C	748	ASN	3.0
1	C	1015	GLY	3.0
1	C	783	ASP	2.9
1	C	417	ARG	2.9
1	A	366	LYS	2.8
2	D	146	LEU	2.8
2	D	69	PHE	2.8
1	C	362	SER	2.7
1	C	429	ARG	2.7
1	C	487	ASN	2.7
1	A	471	HIS	2.7
1	C	419	PHE	2.7
1	A	469	THR	2.7
1	C	392	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	575	ASP	2.7
1	C	751	ASP	2.7
1	C	413	TRP	2.7
1	C	471	HIS	2.6
2	D	109	VAL	2.6
1	C	469	THR	2.6
1	A	1114	LEU	2.6
1	A	749	GLU	2.6
1	C	807	VAL	2.6
2	D	104	GLY	2.6
1	A	808	ARG	2.6
1	C	472	ASP	2.6
1	A	935	ASP	2.6
1	A	1227	GLY	2.5
1	C	412	LEU	2.5
2	D	70	LEU	2.5
2	D	83	ASP	2.5
1	A	1103	GLU	2.5
2	D	115	LEU	2.5
1	A	1186	GLU	2.5
1	C	476	VAL	2.5
1	C	560	GLU	2.5
1	C	779	ILE	2.5
1	C	373	LEU	2.5
1	C	371	ILE	2.4
1	A	384	MET	2.4
1	A	531	ASP	2.4
1	A	429	ARG	2.4
1	A	1193	THR	2.4
1	C	797	GLN	2.4
2	D	105	GLY	2.3
1	A	503	GLN	2.3
1	A	419	PHE	2.3
1	C	1209	GLY	2.3
1	A	1188	LEU	2.2
1	C	793	LEU	2.2
1	C	1150	ARG	2.2
1	C	431	LYS	2.2
1	A	416	ASP	2.2
2	D	71	LEU	2.2
2	D	136	VAL	2.2
1	A	367	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	574	GLY	2.2
1	C	470	LYS	2.2
1	A	395	THR	2.2
1	C	810	LEU	2.1
1	C	384	MET	2.1
2	D	59	VAL	2.1
1	C	590	PHE	2.1
2	B	145	PHE	2.1
1	A	577	LYS	2.1
1	A	1150	ARG	2.1
1	C	745	ARG	2.1
1	A	418	GLU	2.1
1	C	506	PHE	2.1
1	A	829	SER	2.0
2	D	64	ASN	2.0
1	A	648	PHE	2.0
1	A	583	THR	2.0
1	C	539	HIS	2.0
1	A	505	ARG	2.0
1	C	808	ARG	2.0
2	D	74	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

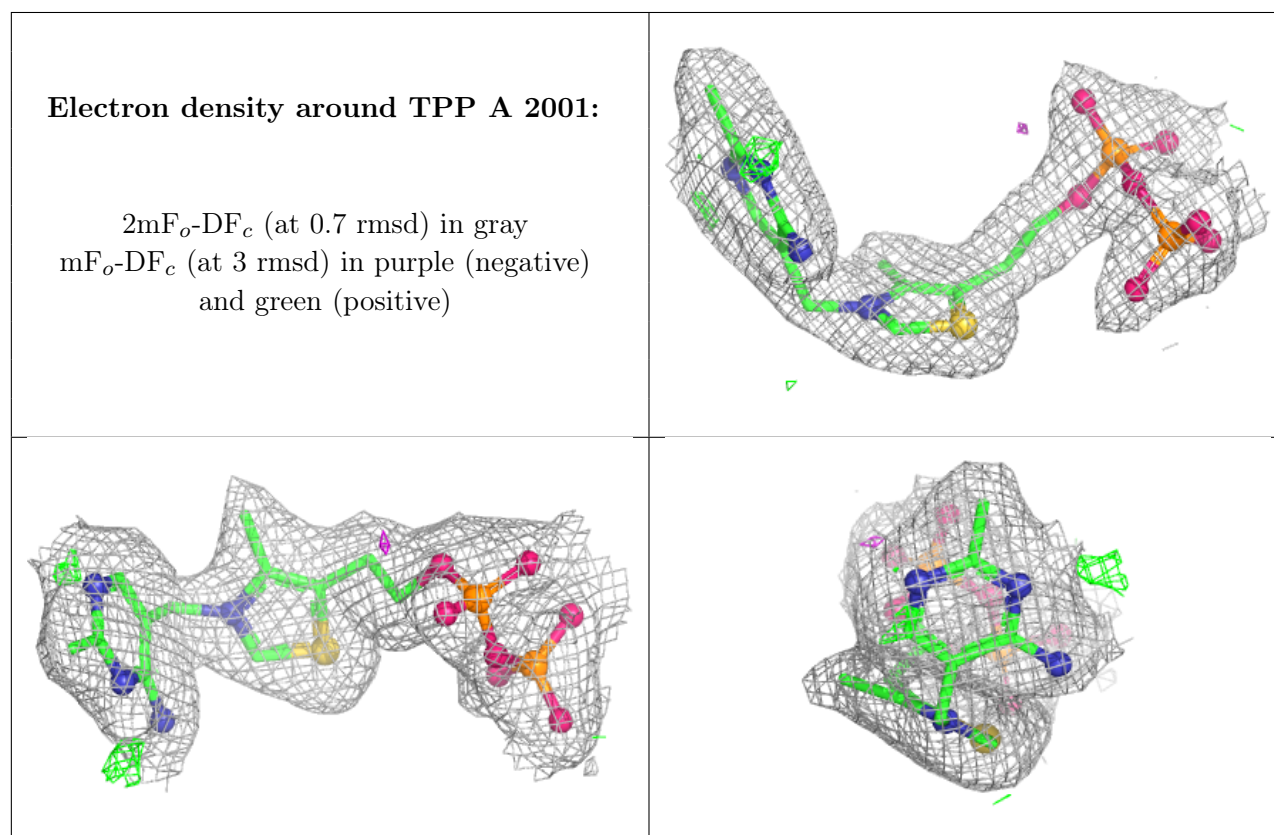
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	TPP	A	2001	26/26	0.97	0.07	17,22,27,27	0
3	TPP	C	2001	26/26	0.98	0.05	18,22,25,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	A	2002	1/1	0.99	0.01	14,14,14,14	0
4	MG	C	2002	1/1	0.99	0.02	17,17,17,17	0
5	CA	A	2003	1/1	0.99	0.07	23,23,23,23	0
5	CA	C	2003	1/1	0.99	0.05	27,27,27,27	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 ⓘ

There are no such residues in this entry.