Full wwPDB X-ray Structure Validation Report (i)

Sep 2, 2023 – 12:16 PM EDT

PDB ID	:	3QV8
Title	:	Crystal structure of Leishmania mexicana pyruvate kinase(LmPYK)in complex with benzothiazole-2,5-disulfonic acid.
Authors	:	Morgan, H.P.; Auld, D.S.; McNae, I.W.; Nowicki, M.W.; Michels, P.A.M.; Fothergill-Gilmore, L.A.; Walkinshaw, M.D.
Deposited on	:	2011-02-25
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 (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 (i)) were used in the production of this report:

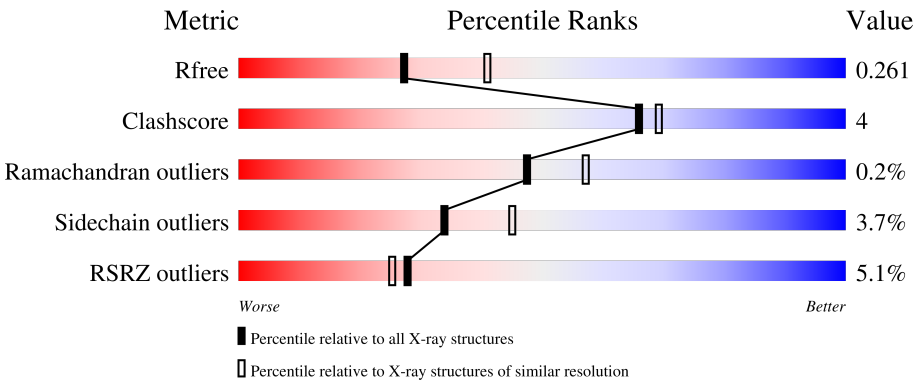
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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 <=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	499	4% 68% 11% • 21%
1	D	499	5% 89% 9% ••

2 Entry composition (i)

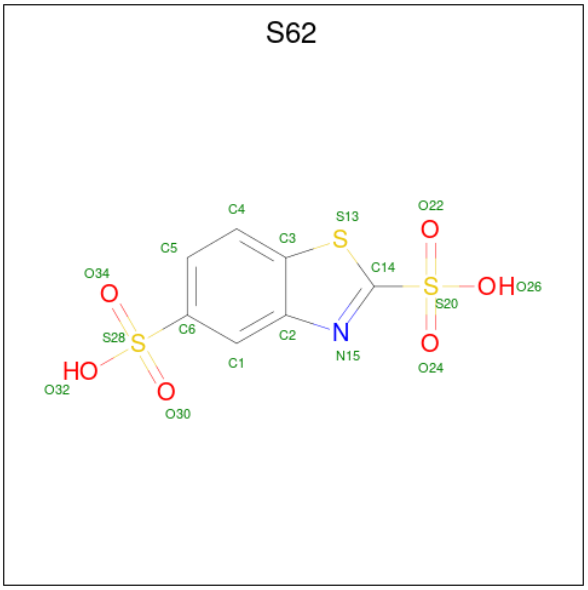
There are 4 unique types of molecules in this entry. The entry contains 7040 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Pyruvate kinase.

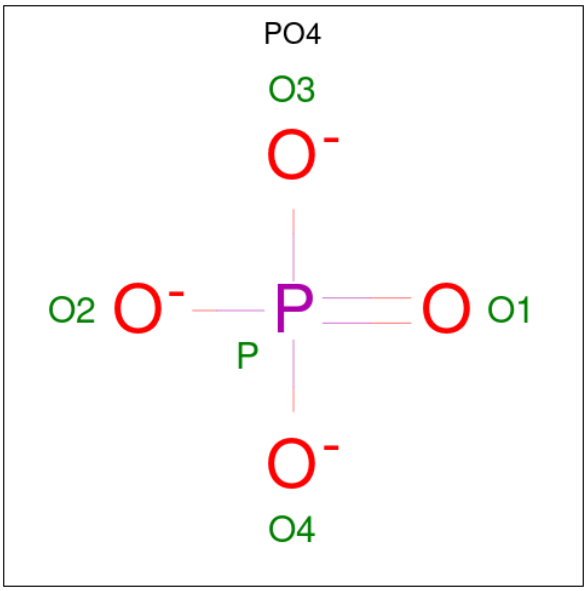
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	492	3764	2347	662	729	26	0	2	0
1	A	396	3011	1880	534	575	22	0	2	0

- Molecule 2 is 1,3-benzothiazole-2,5-disulfonic acid (three-letter code: S62) (formula: $C_7H_5NO_6S_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	D	1	17	7	1	6	3	0	0
2	A	1	17	7	1	6	3	0	0

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



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

- Molecule 4 is water.

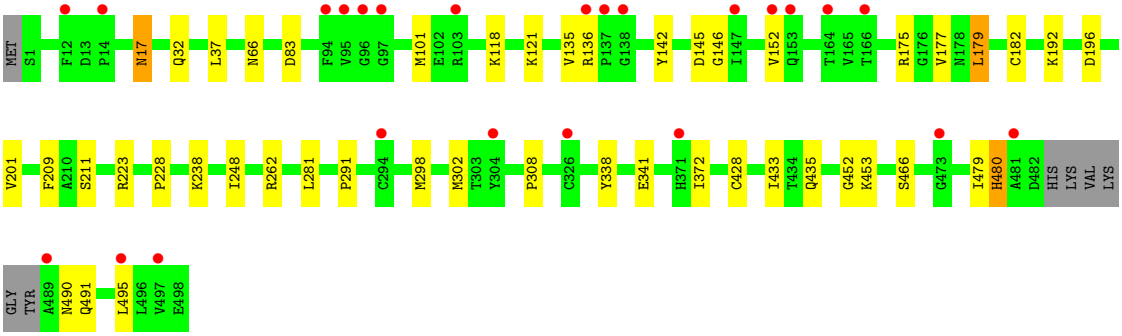
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	97	Total O 97 97	0	0
4	A	114	Total O 114 114	0	0

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.

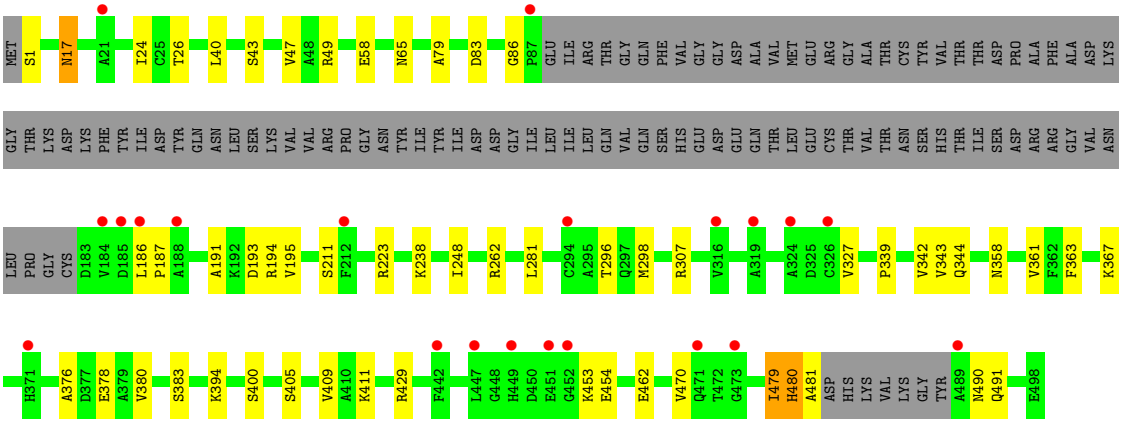
- Molecule 1: Pyruvate kinase

Chain D:



- Molecule 1: Pyruvate kinase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	120.55Å 131.28Å 167.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.41 – 2.45 39.23 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.41-2.45) 99.9 (39.23-2.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.86 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.234 , 0.266 0.228 , 0.261	Depositor DCC
R_{free} test set	2485 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	45.6	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 36.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7040	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PO4, S62

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	0.50	0/3058	0.59	0/4136
1	D	0.49	0/3826	0.58	0/5180
All	All	0.50	0/6884	0.59	0/9316

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	3011	0	3046	31	0
1	D	3764	0	3763	23	0
2	A	17	0	5	1	0
2	D	17	0	5	0	0
3	A	10	0	0	2	0
3	D	10	0	0	0	0
4	A	114	0	0	2	0
4	D	97	0	0	2	0
All	All	7040	0	6819	54	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 (54) 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:D:17:ASN:HD22	1:D:17:ASN:H	0.99	0.95
1:D:17:ASN:H	1:D:17:ASN:ND2	1.79	0.80
1:D:248:ILE:HG12	1:D:281:LEU:HD22	1.70	0.73
1:D:135:VAL:HG11	1:D:152:VAL:HG21	1.73	0.70
1:A:358:ASN:HD22	1:A:361:VAL:HG23	1.56	0.69
1:D:179:LEU:HB3	1:D:182:CYS:HB2	1.73	0.69
1:A:58:GLU:HG3	4:A:519:HOH:O	2.00	0.61
1:A:358:ASN:ND2	1:A:361:VAL:HG23	2.15	0.59
1:D:17:ASN:HD22	1:D:17:ASN:N	1.81	0.59
1:A:248:ILE:HG12	1:A:281:LEU:HD22	1.84	0.59
1:D:142:TYR:HB3	1:D:146:GLY:HA2	1.86	0.57
1:A:298:MET:HE1	1:A:327:VAL:HG12	1.86	0.56
1:D:452:GLY:O	1:D:453:LYS:HB2	2.06	0.56
1:A:394:LYS:HB2	1:A:470:VAL:HG12	1.89	0.55
1:A:211:SER:HA	1:A:238:LYS:HD3	1.89	0.54
1:D:291:PRO:HB3	1:D:433:ILE:O	2.08	0.53
1:D:223:ARG:HD2	4:D:513:HOH:O	2.07	0.53
1:A:376:ALA:O	1:A:380:VAL:HG23	2.09	0.53
1:A:86:GLY:HA2	1:A:193:ASP:OD2	2.09	0.53
1:A:17:ASN:HD22	1:A:17:ASN:N	2.07	0.53
1:D:211:SER:HA	1:D:238:LYS:HD3	1.93	0.51
1:A:400:SER:OG	3:A:501:PO4:O2	2.22	0.50
1:A:65:ASN:HB3	4:A:615:HOH:O	2.11	0.50
1:A:363:PHE:CZ	1:A:367:LYS:HD2	2.47	0.50
1:A:186:LEU:HB3	1:A:187:PRO:HD2	1.94	0.49
1:D:37:LEU:HD12	1:D:66:ASN:HB3	1.94	0.48
1:D:302:MET:SD	1:D:308:PRO:HD3	2.53	0.48
1:A:79:ALA:HB2	1:A:429:ARG:O	2.14	0.47
1:A:378:GLU:OE2	1:A:411:LYS:NZ	2.46	0.47
1:A:339:PRO:O	1:A:343:VAL:HG23	2.16	0.46
1:D:490:ASN:OD1	1:D:491:GLN:N	2.50	0.45
1:D:101:MET:HE1	1:D:121:LYS:HA	1.98	0.45
1:A:43:SER:HB3	1:A:344:GLN:HG3	1.98	0.45
1:A:380:VAL:HG12	1:A:479:ILE:HD12	1.98	0.45
1:A:405:SER:O	1:A:409:VAL:HG23	2.17	0.45
1:A:24:ILE:HG12	1:A:47:VAL:HB	1.99	0.45
1:D:428:CYS:HB3	4:D:569:HOH:O	2.16	0.44
1:A:1:SER:HB3	3:A:500:PO4:O2	2.18	0.44
1:A:191:ALA:O	1:A:195:VAL:HG23	2.19	0.43
1:D:338:TYR:HB3	1:D:341:GLU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:ALA:HA	1:A:490:ASN:HA	2.01	0.43
1:A:339:PRO:O	1:A:342:VAL:HG12	2.19	0.42
1:A:480[A]:HIS:CD2	1:A:491:GLN:HB2	2.54	0.42
1:D:83:ASP:HA	1:D:209:PHE:HB2	2.01	0.42
1:D:192:LYS:HG2	1:D:196:ASP:OD2	2.19	0.42
1:D:32:GLN:O	1:D:66:ASN:ND2	2.53	0.42
1:D:490:ASN:O	1:D:491:GLN:HB2	2.20	0.42
1:A:49:ARG:NH2	1:A:83:ASP:OD2	2.38	0.41
1:A:26:THR:HG21	2:A:499:S62:O24	2.21	0.41
1:A:194:ARG:NH1	1:A:194:ARG:HB2	2.37	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	392/499 (79%)	383 (98%)	8 (2%)	1 (0%)	41	49
1	D	490/499 (98%)	464 (95%)	25 (5%)	1 (0%)	47	57
All	All	882/998 (88%)	847 (96%)	33 (4%)	2 (0%)	47	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	296	THR
1	D	201	VAL

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	330/417 (79%)	318 (96%)	12 (4%)	35	46
1	D	413/417 (99%)	396 (96%)	17 (4%)	30	40
All	All	743/834 (89%)	714 (96%)	29 (4%)	34	42

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	17	ASN
1	D	118	LYS
1	D	136	ARG
1	D	145	ASP
1	D	175	ARG
1	D	177	VAL
1	D	179	LEU
1	D	228	PRO
1	D	262	ARG
1	D	298	MET
1	D	372	ILE
1	D	435	GLN
1	D	466	SER
1	D	479	ILE
1	D	480[A]	HIS
1	D	480[B]	HIS
1	D	495	LEU
1	A	17	ASN
1	A	40	LEU
1	A	223	ARG
1	A	262	ARG
1	A	307	ARG
1	A	383	SER
1	A	453	LYS
1	A	454	GLU
1	A	462	GLU
1	A	479	ILE
1	A	480[A]	HIS
1	A	480[B]	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	17	ASN
1	D	66	ASN
1	D	159	GLN
1	D	178	ASN
1	D	286	ASN
1	D	305	ASN
1	D	344	GLN
1	D	435	GLN
1	D	471	GLN
1	A	17	ASN
1	A	305	ASN
1	A	491	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)

6 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	PO4	D	500	-	4,4,4	1.02	0	6,6,6	0.52	0
2	S62	D	499	-	15,18,18	3.55	4 (26%)	18,29,29	1.09	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	S62	A	499	-	15,18,18	3.23	4 (26%)	18,29,29	1.13	1 (5%)
3	PO4	A	501	-	4,4,4	0.92	0	6,6,6	0.58	0
3	PO4	D	501	-	4,4,4	0.89	0	6,6,6	0.62	0
3	PO4	A	500	-	4,4,4	1.04	0	6,6,6	0.47	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
2	S62	D	499	-	-	0/6/12/12	0/2/2/2
2	S62	A	499	-	-	0/6/12/12	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	499	S62	C14-S20	-10.05	1.64	1.78
2	A	499	S62	C14-S20	-8.89	1.66	1.78
2	D	499	S62	C6-S28	-8.08	1.60	1.77
2	A	499	S62	C6-S28	-7.54	1.61	1.77
2	D	499	S62	C1-C2	-2.23	1.38	1.41
2	D	499	S62	C2-C3	2.20	1.49	1.42
2	A	499	S62	C1-C6	2.20	1.40	1.36
2	A	499	S62	C2-C3	2.14	1.49	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	499	S62	C1-C2-C3	-3.64	117.05	121.04
2	D	499	S62	C1-C2-C3	-2.77	118.00	121.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	499	S62	1	0
3	A	501	PO4	1	0

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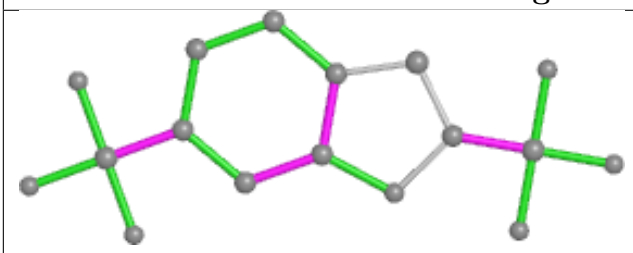
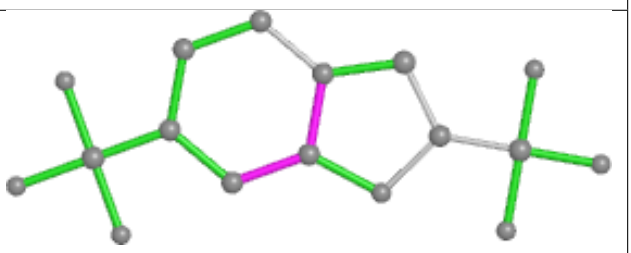
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	500	PO4	1	0

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.

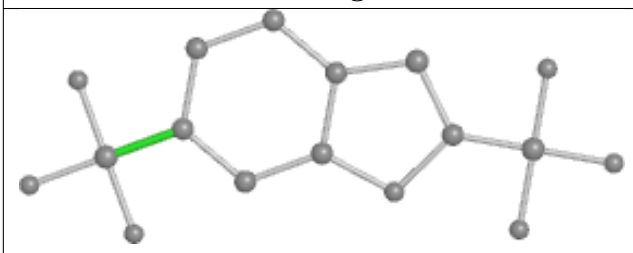
Ligand S62 D 499



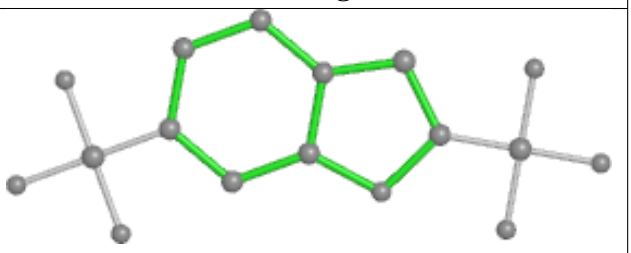
Bond lengths



Bond angles

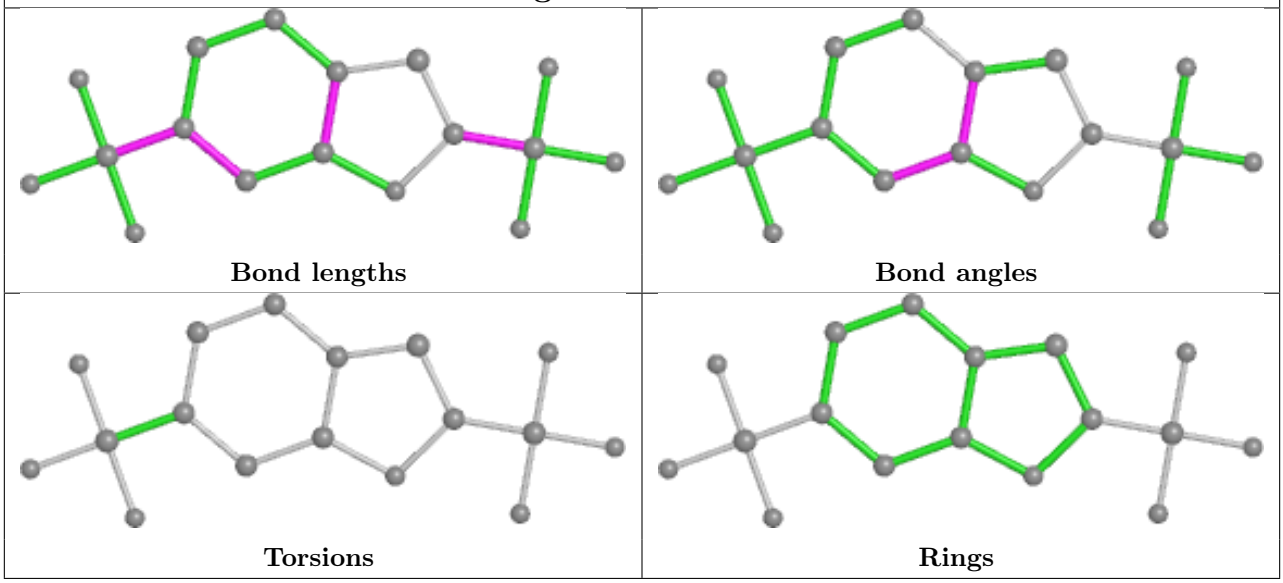


Torsions



Rings

Ligand S62 A 499



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, 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	396/499 (79%)	0.29	21 (5%)	26	23	31, 47, 67, 85	0
1	D	492/499 (98%)	0.28	24 (4%)	29	27	30, 54, 73, 81	0
All	All	888/998 (88%)	0.28	45 (5%)	28	25	30, 51, 73, 85	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	184	VAL	5.8
1	A	186	LEU	3.9
1	D	489	ALA	3.7
1	A	489	ALA	3.5
1	A	452	GLY	3.5
1	D	153	GLN	3.4
1	A	185	ASP	3.4
1	A	87	PRO	3.2
1	D	495	LEU	3.0
1	A	451	GLU	2.9
1	D	94	PHE	2.9
1	D	96	GLY	2.9
1	D	304	TYR	2.8
1	D	481	ALA	2.7
1	A	21	ALA	2.7
1	D	166	THR	2.6
1	A	324	ALA	2.6
1	A	442	PHE	2.6
1	A	316	VAL	2.5
1	A	326	CYS	2.4
1	D	497	VAL	2.4
1	D	294	CYS	2.4
1	A	473	GLY	2.4
1	A	294	CYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	137	PRO	2.3
1	D	103	ARG	2.3
1	D	326	CYS	2.3
1	D	371	HIS	2.3
1	D	95	VAL	2.3
1	D	152	VAL	2.2
1	A	447	LEU	2.2
1	D	138	GLY	2.2
1	A	319	ALA	2.2
1	A	449	HIS	2.2
1	A	212	PHE	2.2
1	D	147	ILE	2.2
1	A	471	GLN	2.1
1	D	12	PHE	2.1
1	A	371	HIS	2.1
1	D	473	GLY	2.1
1	D	136	ARG	2.1
1	D	97	GLY	2.1
1	A	188	ALA	2.0
1	D	164	THR	2.0
1	D	14	PRO	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(Å^2)	Q<0.9
2	S62	D	499	17/17	0.79	0.22	100,104,107,107	0
2	S62	A	499	17/17	0.90	0.18	83,87,90,91	0

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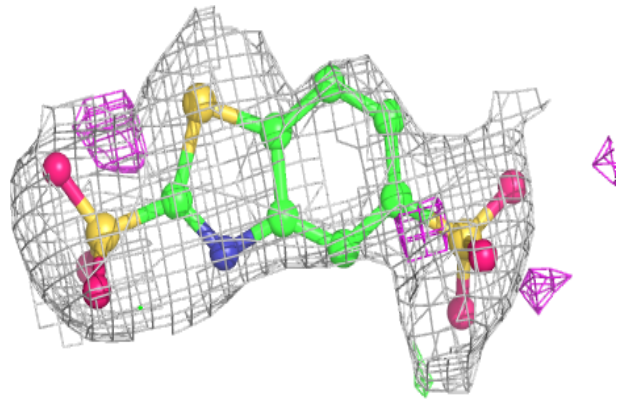
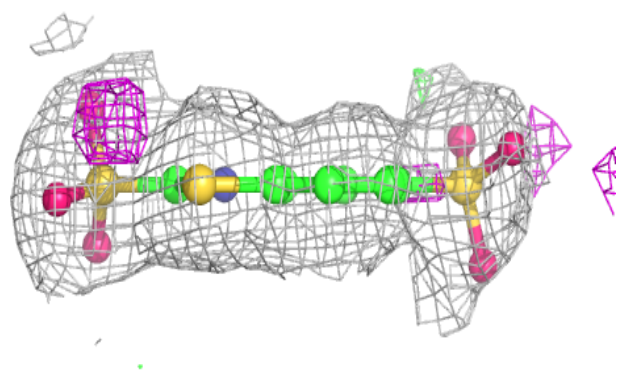
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PO4	A	501	5/5	0.93	0.13	85,85,86,87	0
3	PO4	A	500	5/5	0.94	0.17	66,66,67,67	0
3	PO4	D	501	5/5	0.96	0.18	63,64,66,66	0
3	PO4	D	500	5/5	0.97	0.15	72,73,74,75	0

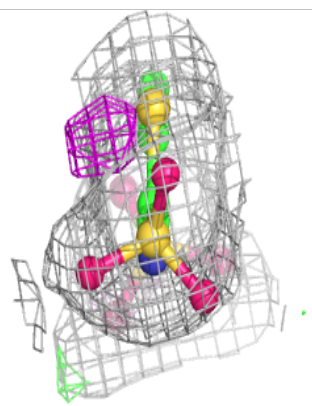
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around S62 D 499:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

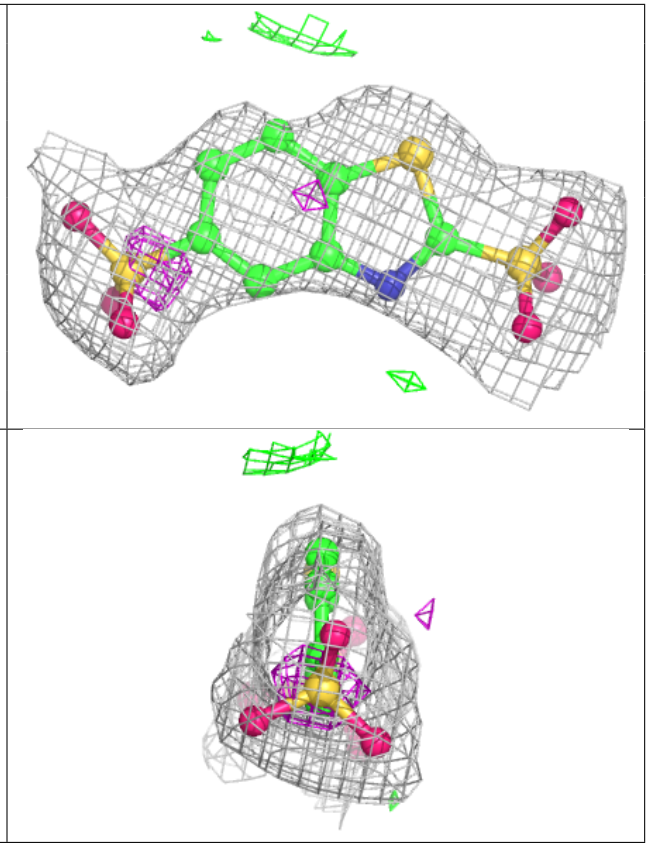






Electron density around S62 A 499:

$2mF_o$-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.