Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 01:30 PM EST

PDB ID	:	4OWO
Title	:	Anthranilate phosphoribosyl transferase from Mycobacterium tuberculosis in complex with 6-fluoroanthranilate, PRPP and Magnesium
Authors	:	Castell, A.; Cookson, T.V.M.; Short, F.L.; Lott, J.S.
Deposited on	:	2014-02-02
Resolution	:	1.99 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:

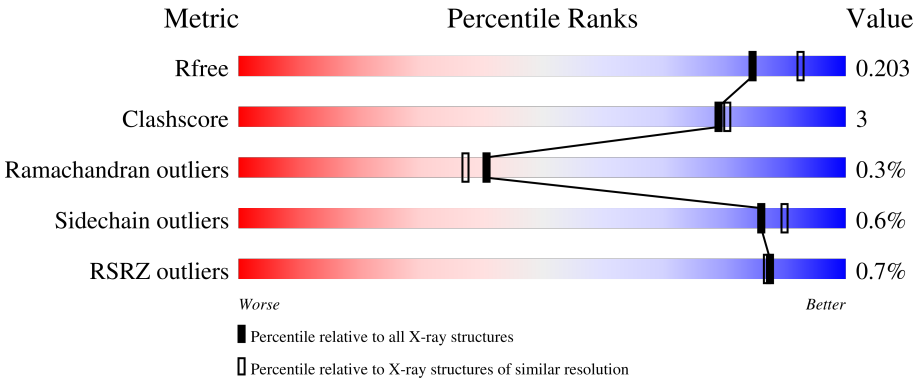
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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-RAY DIFFRACTION

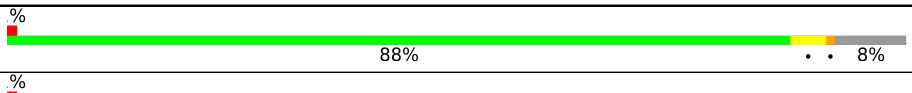
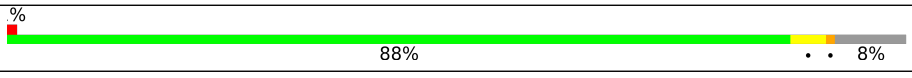
The reported resolution of this entry is 1.99 Å.

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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	378	
1	B	378	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5642 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 Anthranilate phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	348	Total 2507	C 1569	N 463	O 466	S 9	0	1	0
1	B	349	Total 2507	C 1570	N 462	O 466	S 9	0	0	0

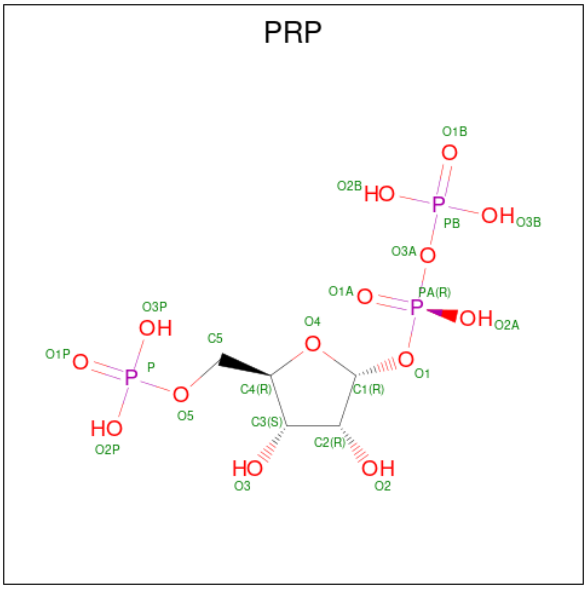
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	371	LEU	-	expression tag	UNP P66992
A	372	GLU	-	expression tag	UNP P66992
A	373	HIS	-	expression tag	UNP P66992
A	374	HIS	-	expression tag	UNP P66992
A	375	HIS	-	expression tag	UNP P66992
A	376	HIS	-	expression tag	UNP P66992
A	377	HIS	-	expression tag	UNP P66992
A	378	HIS	-	expression tag	UNP P66992
B	371	LEU	-	expression tag	UNP P66992
B	372	GLU	-	expression tag	UNP P66992
B	373	HIS	-	expression tag	UNP P66992
B	374	HIS	-	expression tag	UNP P66992
B	375	HIS	-	expression tag	UNP P66992
B	376	HIS	-	expression tag	UNP P66992
B	377	HIS	-	expression tag	UNP P66992
B	378	HIS	-	expression tag	UNP P66992

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

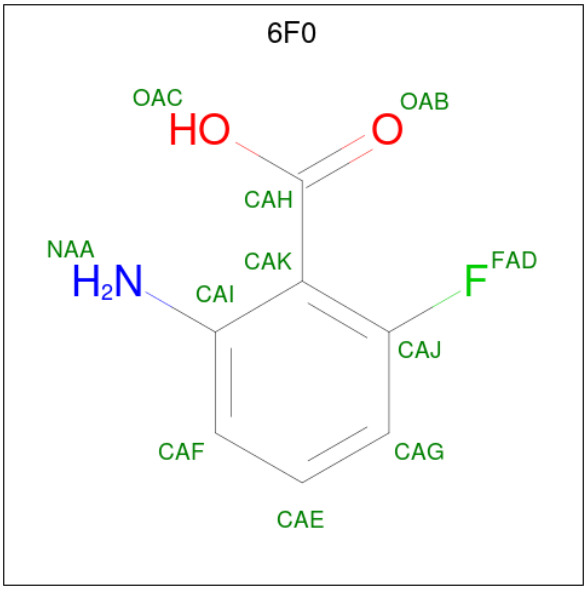
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Mg 2	0	0
2	B	2	Total 2	Mg 2	0	0

- Molecule 3 is 1-O-pyrophosphono-5-O-phosphono-alpha-D-ribofuranose (three-letter code: PRP) (formula: $C_5H_{13}O_{14}P_3$).



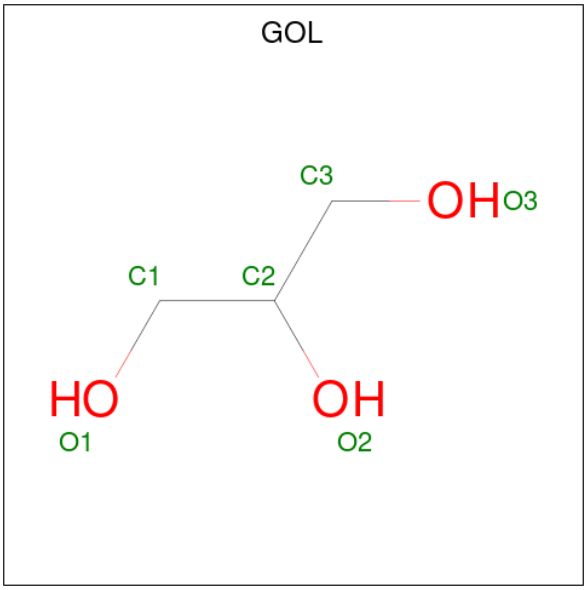
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			22	5	14	3		
3	B	1	Total	C	O	P	0	0
			22	5	14	3		

- Molecule 4 is 2-azanyl-6-fluoranyl-benzoic acid (three-letter code: 6F0) (formula: $C_7H_6FNO_2$).



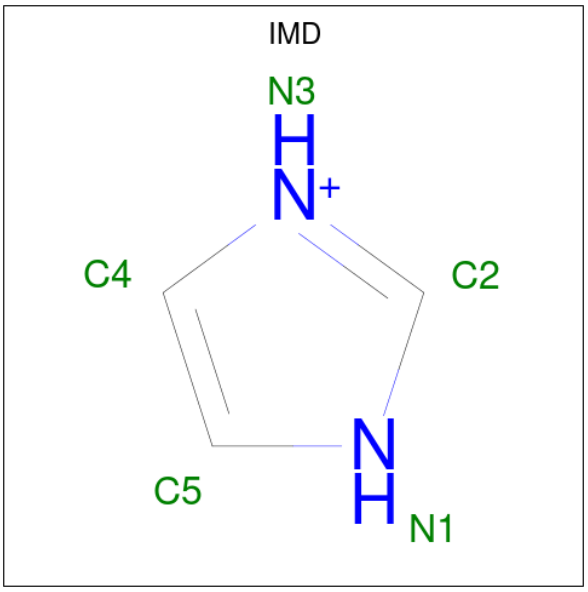
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			11	7	1	1	2		
4	A	1	Total	C	F	N	O	0	0
			11	7	1	1	2		
4	B	1	Total	C	F	N	O	0	0
			11	7	1	1	2		
4	B	1	Total	C	F	N	O	0	0
			11	7	1	1	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C N 5 3 2	0	0

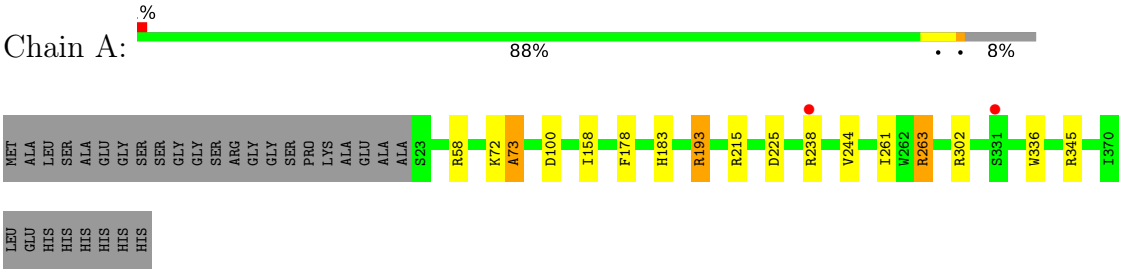
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	264	Total O 264 264	0	0
7	B	249	Total O 249 249	0	0

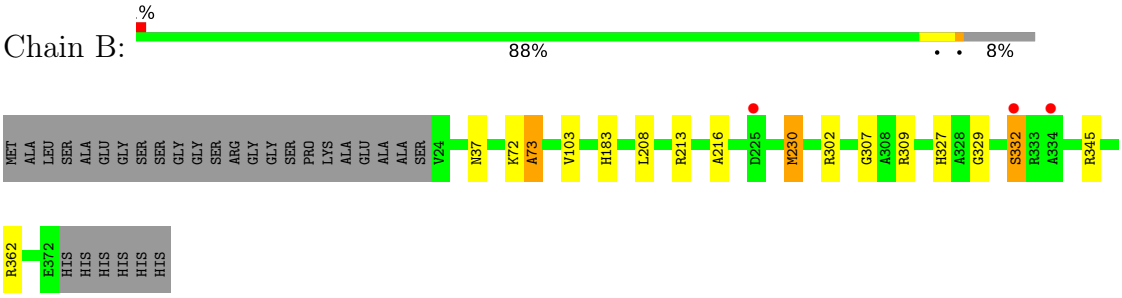
3 Residue-property plots (i)

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: Anthranilate phosphoribosyltransferase



• Molecule 1: Anthranilate phosphoribosyltransferase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.41Å 92.10Å 121.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.35 – 1.99 66.44 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.6 (73.35-1.99) 99.7 (66.44-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.16 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.161 , 0.194 0.172 , 0.203	Depositor DCC
R_{free} test set	3110 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	23.0	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 47.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5642	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 6F0, PRP, GOL, IMD

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	0/2558	0.68	1/3493 (0.0%)
1	B	0.45	0/2555	0.68	1/3490 (0.0%)
All	All	0.46	0/5113	0.68	2/6983 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	345	ARG	NE-CZ-NH2	5.13	122.86	120.30
1	A	263	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	332	SER	Peptide

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	2507	0	2488	17	0
1	B	2507	0	2488	11	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	22	0	8	0	0
3	B	22	0	8	0	0
4	A	22	0	10	1	0
4	B	22	0	10	1	0
5	A	12	0	16	0	0
5	B	6	0	8	0	0
6	B	5	0	5	0	0
7	A	264	0	0	6	0
7	B	249	0	0	3	0
All	All	5642	0	5041	28	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 3.

All (28) 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:B:307:GLY:O	1:B:309:ARG:NH1	2.25	0.69
1:A:263:ARG:HD3	1:A:336:TRP:CZ3	2.33	0.64
1:A:238:ARG:HA	7:A:582:HOH:O	2.00	0.61
1:A:263:ARG:HD2	7:A:573:HOH:O	2.02	0.60
1:B:302:ARG:NH2	7:B:501:HOH:O	2.39	0.55
1:A:193:ARG:HG2	7:A:658:HOH:O	2.08	0.52
1:B:72:LYS:O	1:B:73:ALA:CB	2.58	0.52
1:B:103:VAL:HG12	1:B:216:ALA:HB3	1.92	0.51
1:A:225:ASP:OD1	1:A:225:ASP:N	2.42	0.51
1:B:103:VAL:HG11	1:B:327:HIS:HB2	1.93	0.51
1:B:72:LYS:O	1:B:73:ALA:HB3	2.14	0.48
1:A:158:ILE:O	1:A:178:PHE:HB2	2.15	0.46
1:A:193:ARG:HG3	7:A:595:HOH:O	2.13	0.46
1:B:208:LEU:HD21	1:B:230:MET:HG3	1.98	0.46
1:A:72:LYS:O	1:A:73:ALA:CB	2.64	0.46
1:B:183:HIS:HB2	4:B:404:6F0:H2	1.98	0.45
1:B:329:GLY:HA2	1:B:332:SER:HB3	1.97	0.45
1:B:213:ARG:NH2	7:B:502:HOH:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:VAL:HG12	1:A:261:ILE:HG12	1.99	0.44
1:A:345[A]:ARG:HH11	1:A:345[A]:ARG:HG2	1.83	0.43
1:A:100:ASP:O	1:A:215:ARG:NH1	2.52	0.43
1:A:72:LYS:O	1:A:73:ALA:HB3	2.19	0.42
1:A:72:LYS:HE3	1:A:72:LYS:HB3	1.93	0.42
1:A:302:ARG:HD3	7:A:711:HOH:O	2.19	0.42
1:B:362:ARG:NH2	7:B:725:HOH:O	2.50	0.42
1:A:345[A]:ARG:HG2	1:A:345[A]:ARG:NH1	2.36	0.41
1:A:58:ARG:NH1	7:A:747:HOH:O	2.53	0.41
1:A:183:HIS:HB2	4:A:404:6F0:H2	2.03	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	347/378 (92%)	338 (97%)	8 (2%)	1 (0%)	41	37
1	B	347/378 (92%)	337 (97%)	9 (3%)	1 (0%)	41	37
All	All	694/756 (92%)	675 (97%)	17 (2%)	2 (0%)	41	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	ALA
1	A	73	ALA

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	241/265 (91%)	240 (100%)	1 (0%)	91 93
1	B	241/265 (91%)	239 (99%)	2 (1%)	81 86
All	All	482/530 (91%)	479 (99%)	3 (1%)	86 90

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	193	ARG
1	B	37	ASN
1	B	230	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	$\#\|Z\|>2$
5	GOL	A	406	-	5,5,5	0.31	0	5,5,5	0.89	0
3	PRP	B	403	2	19,22,22	0.56	0	33,35,35	1.22	3 (9%)
4	6F0	B	405	-	11,11,11	1.33	1 (9%)	13,15,15	1.39	3 (23%)
4	6F0	A	404	-	11,11,11	1.39	1 (9%)	13,15,15	1.87	5 (38%)
6	IMD	B	407	-	3,5,5	0.29	0	4,5,5	0.60	0
3	PRP	A	403	2	19,22,22	0.61	0	33,35,35	1.51	5 (15%)
5	GOL	B	406	-	5,5,5	0.41	0	5,5,5	1.09	0
4	6F0	B	404	-	11,11,11	1.49	1 (9%)	13,15,15	1.88	6 (46%)
5	GOL	A	407	-	5,5,5	0.45	0	5,5,5	0.45	0
4	6F0	A	405	-	11,11,11	1.41	1 (9%)	13,15,15	1.38	3 (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
5	GOL	A	406	-	-	1/4/4/4	-
3	PRP	B	403	2	-	6/16/33/33	0/1/1/1
4	6F0	B	405	-	-	2/4/4/4	0/1/1/1
4	6F0	A	404	-	-	2/4/4/4	0/1/1/1
6	IMD	B	407	-	-	-	0/1/1/1
3	PRP	A	403	2	-	9/16/33/33	0/1/1/1
5	GOL	B	406	-	-	4/4/4/4	-
4	6F0	B	404	-	-	0/4/4/4	0/1/1/1
5	GOL	A	407	-	-	4/4/4/4	-
4	6F0	A	405	-	-	2/4/4/4	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	404	6F0	CAK-CAH	-3.79	1.41	1.50
4	A	404	6F0	CAK-CAH	-3.58	1.41	1.50
4	B	405	6F0	CAK-CAH	-3.40	1.42	1.50
4	A	405	6F0	CAK-CAH	-3.29	1.42	1.50

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	403	PRP	PA-O1-C1	4.18	135.91	119.74
3	A	403	PRP	O1-PA-O1A	-4.01	94.43	109.47
4	B	404	6F0	CAF-CAI-CAK	3.27	122.71	118.29
4	A	404	6F0	FAD-CAJ-CAK	3.20	123.00	118.01
4	A	404	6F0	CAF-CAI-CAK	3.12	122.51	118.29
3	A	403	PRP	O2A-PA-O1	2.86	118.08	106.78
4	B	404	6F0	CAK-CAI-NAA	-2.85	117.79	121.66
4	B	404	6F0	CAE-CAG-CAJ	2.52	122.60	118.46
4	A	404	6F0	CAK-CAI-NAA	-2.47	118.31	121.66
3	B	403	PRP	PA-O1-C1	2.46	129.25	119.74
3	B	403	PRP	O3A-PB-O1B	-2.44	97.63	111.19
4	B	404	6F0	FAD-CAJ-CAK	2.37	121.71	118.01
4	A	404	6F0	CAE-CAG-CAJ	2.31	122.25	118.46
4	A	405	6F0	CAK-CAI-NAA	-2.31	118.52	121.66
3	A	403	PRP	O3B-PB-O2B	2.31	116.47	107.64
4	A	405	6F0	OAC-CAH-OAB	-2.30	118.24	123.35
4	B	405	6F0	OAC-CAH-CAK	2.28	121.35	114.75
4	A	405	6F0	CAF-CAI-CAK	2.20	121.26	118.29
4	B	405	6F0	CAF-CAI-CAK	2.18	121.23	118.29
3	B	403	PRP	O3B-PB-O2B	2.17	115.94	107.64
4	A	404	6F0	CAG-CAJ-CAK	-2.15	119.74	123.58
4	B	404	6F0	CAG-CAJ-CAK	-2.12	119.78	123.58
3	A	403	PRP	O2A-PA-O1A	2.08	122.54	112.24
4	B	405	6F0	OAC-CAH-OAB	-2.08	118.73	123.35
4	B	404	6F0	OAC-CAH-CAK	2.02	120.61	114.75

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	PRP	C1-O1-PA-O2A
3	A	403	PRP	PA-O3A-PB-O3B
3	B	403	PRP	PA-O3A-PB-O3B
4	B	405	6F0	OAB-CAH-CAK-CAI
4	B	405	6F0	OAC-CAH-CAK-CAI
5	A	407	GOL	O1-C1-C2-C3
5	A	407	GOL	C1-C2-C3-O3
5	B	406	GOL	O1-C1-C2-C3
5	B	406	GOL	C1-C2-C3-O3
5	B	406	GOL	O2-C2-C3-O3
5	A	407	GOL	O1-C1-C2-O2
5	A	407	GOL	O2-C2-C3-O3
5	B	406	GOL	O1-C1-C2-O2

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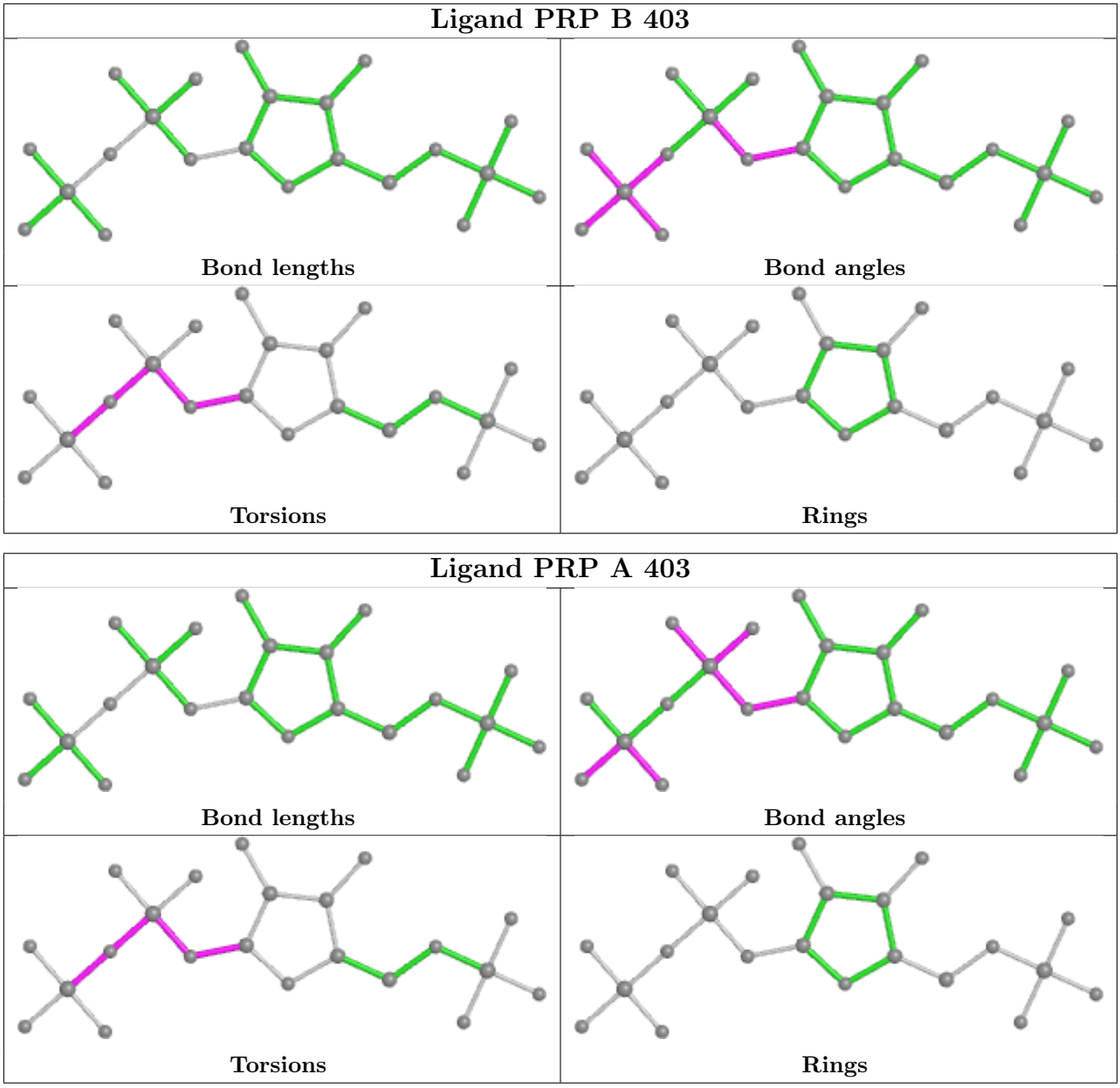
Mol	Chain	Res	Type	Atoms
3	A	403	PRP	C1-O1-PA-O3A
3	A	403	PRP	PB-O3A-PA-O1A
3	B	403	PRP	C1-O1-PA-O3A
5	A	406	GOL	O1-C1-C2-O2
3	A	403	PRP	C1-O1-PA-O1A
3	A	403	PRP	PB-O3A-PA-O2A
4	A	404	6F0	OAC-CAH-CAK-CAI
4	A	405	6F0	OAB-CAH-CAK-CAI
4	A	405	6F0	OAC-CAH-CAK-CAI
3	A	403	PRP	PA-O3A-PB-O1B
3	B	403	PRP	PA-O3A-PB-O1B
3	A	403	PRP	PA-O3A-PB-O2B
3	B	403	PRP	PA-O3A-PB-O2B
3	B	403	PRP	PB-O3A-PA-O1A
4	A	404	6F0	OAB-CAH-CAK-CAI
3	A	403	PRP	C2-C1-O1-PA
3	B	403	PRP	C2-C1-O1-PA

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	6F0	1	0
4	B	404	6F0	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

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, 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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	348/378 (92%)	-0.01	2 (0%)	89	88	12, 22, 41, 60	0
1	B	349/378 (92%)	0.02	3 (0%)	84	83	13, 22, 40, 71	0
All	All	697/756 (92%)	0.00	5 (0%)	87	87	12, 22, 41, 71	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	331	SER	3.9
1	A	238	ARG	3.3
1	B	332	SER	2.5
1	B	334	ALA	2.4
1	B	225	ASP	2.1

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 monosaccharides in this entry.

6.4 Ligands

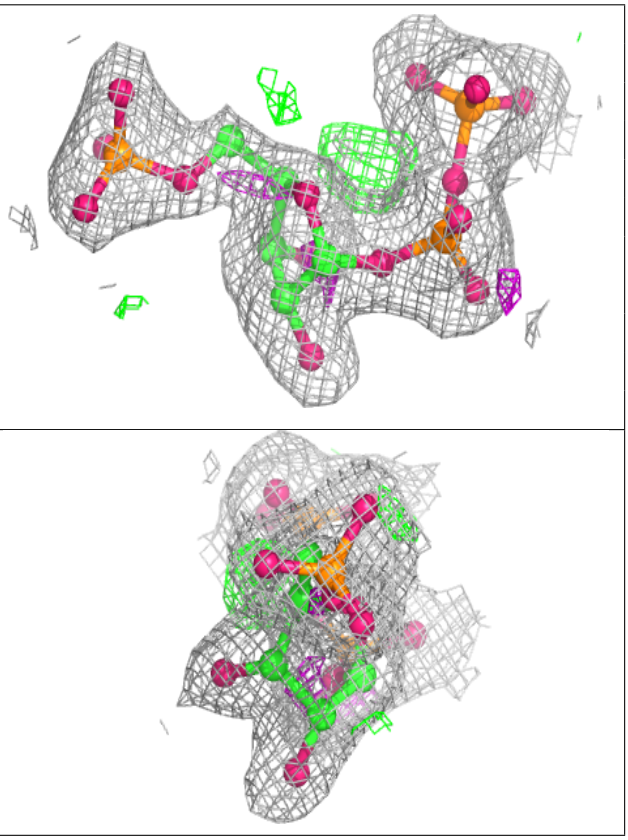
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

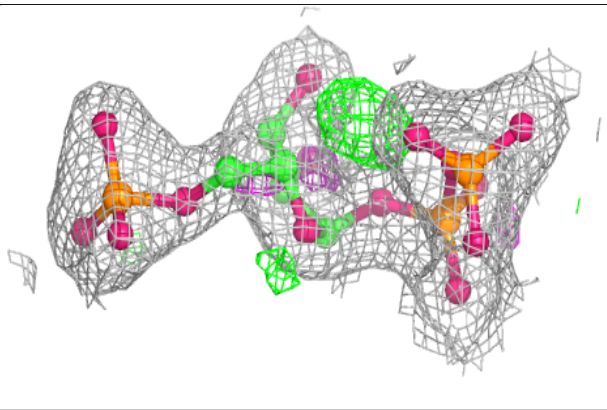
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	GOL	A	407	6/6	0.72	0.19	45,49,51,55	0
4	6F0	A	404	11/11	0.82	0.20	36,38,42,42	0
6	IMD	B	407	5/5	0.82	0.20	47,47,48,48	0
5	GOL	B	406	6/6	0.84	0.22	39,39,41,42	0
4	6F0	B	404	11/11	0.92	0.18	31,32,32,33	0
5	GOL	A	406	6/6	0.93	0.12	27,28,31,33	0
4	6F0	A	405	11/11	0.96	0.11	20,22,22,22	0
4	6F0	B	405	11/11	0.96	0.10	24,24,26,26	0
3	PRP	A	403	22/22	0.97	0.13	20,33,38,39	0
3	PRP	B	403	22/22	0.98	0.11	20,29,34,37	0
2	MG	B	402	1/1	0.98	0.07	35,35,35,35	0
2	MG	A	401	1/1	0.98	0.06	29,29,29,29	0
2	MG	B	401	1/1	0.99	0.06	20,20,20,20	0
2	MG	A	402	1/1	0.99	0.08	18,18,18,18	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 PRP A 403:

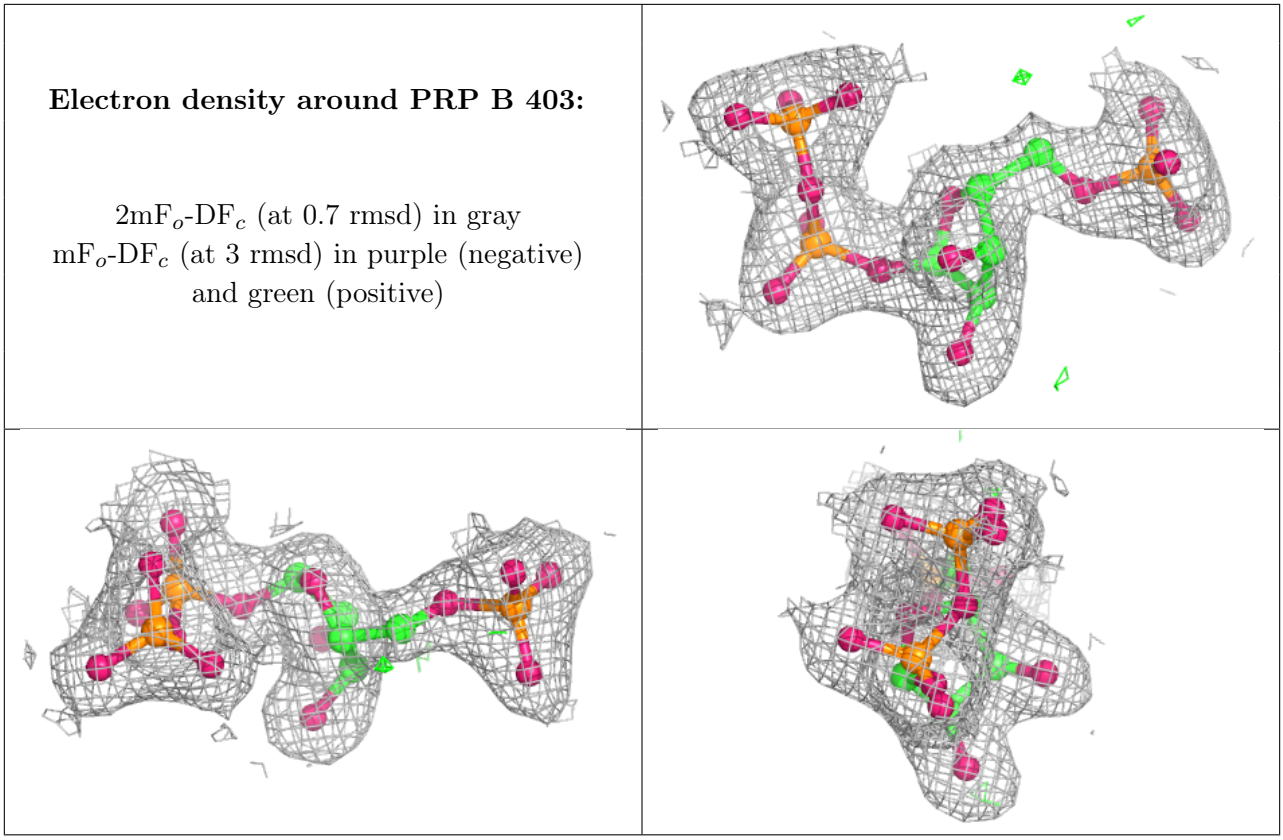
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around PRP B 403:

$2mF_o$-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.