wwPDB X-ray Structure Validation Summary Report (i)

Nov 1, 2023 – 01:33 PM JST

PDB ID	:	5I3S
Title	:	Crystal structure of Staphylococcal IMPase-II
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Deposited on	:	2016-02-11
Resolution	:	2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

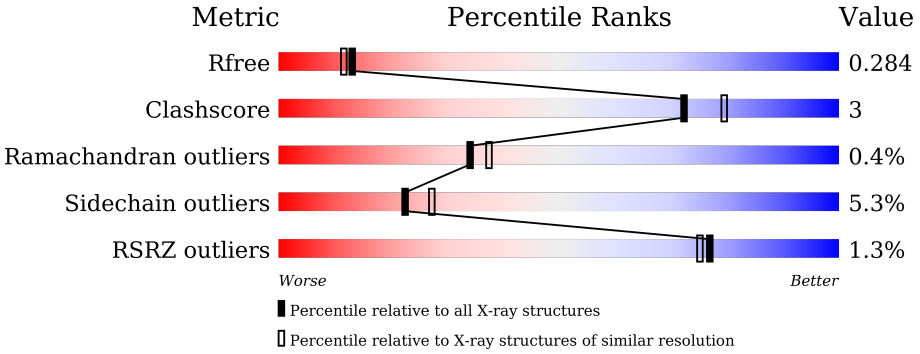
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 <=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	275	.% 82% 11% • 5%
1	B	275	.% 84% 8% • 6%
1	C	275	2% 84% 9% • 6%
1	D	275	.% 80% 8% • 9%

2 Entry composition (i)

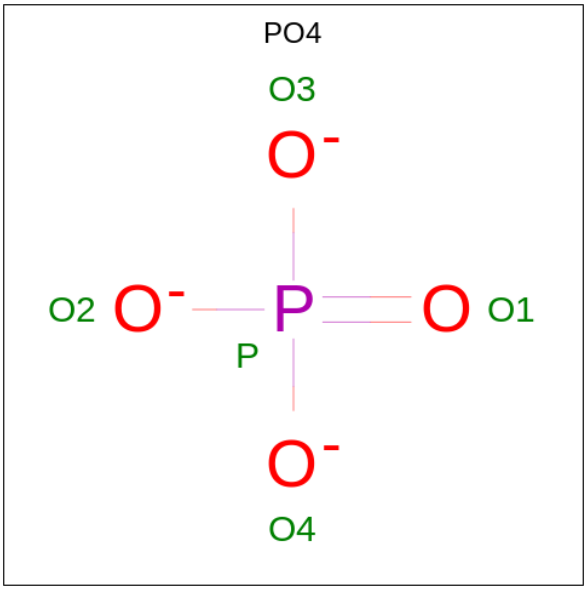
There are 3 unique types of molecules in this entry. The entry contains 8200 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Inositol monophosphatase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	1996	1274	336	383	3	0	0	0
1	B	258	1942	1241	324	374	3	0	0	0
1	C	258	1971	1260	332	376	3	0	0	0
1	D	249	1867	1193	311	360	3	0	0	0

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	C	1	5	4	1	0	0
			Total	O	P		
2	D	1	5	4	1	0	0

- Molecule 3 is water.

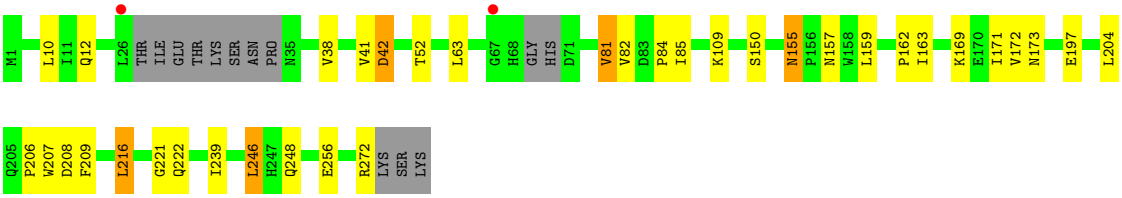
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	107	107	107	0	0
			Total	O		
3	B	95	95	95	0	0
			Total	O		
3	C	98	98	98	0	0
			Total	O		
3	D	104	104	104	0	0

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.

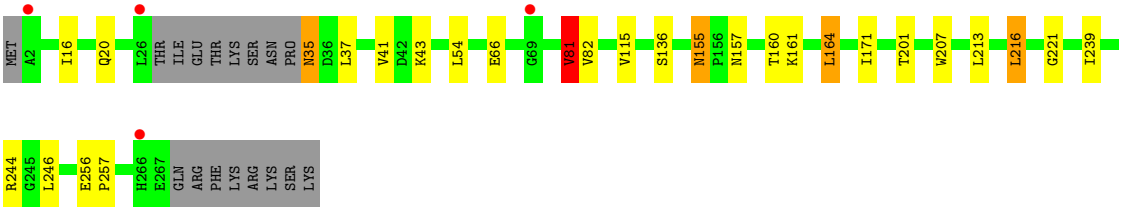
• Molecule 1: Inositol monophosphatase family protein

Chain A:



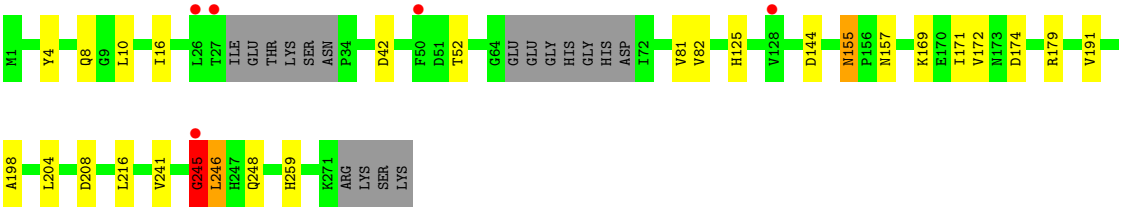
• Molecule 1: Inositol monophosphatase family protein

Chain B:



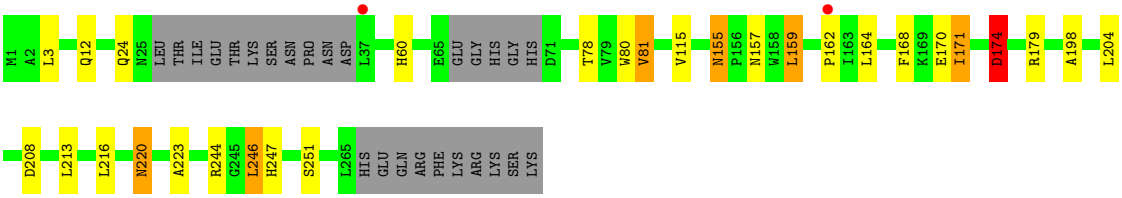
• Molecule 1: Inositol monophosphatase family protein

Chain C:



• Molecule 1: Inositol monophosphatase family protein

Chain D:


M1
A2
L3
Q12
Q24
N25
LEU
THR
ILE
GLU
THR
LYS
SER
ASN
PRO
ASN
ASP
L37
H60
E65
GLU
GLY
HIS
GLY
HIS
D71
T78
V79
W80
V81
V115
N155
P156
N157
W158
L159
P162
I163
L164
F168
K169
E170
I171
D174
R179
A198
L204
D208
L213
L216
N220
A223
R244
G245
L246
H247
S251
L265
HIS
GLU
GLN
ARG
PHE
LYS
ARG
LYS
SER
LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	56.00Å 131.39Å 80.90Å 90.00° 104.43° 90.00°	Depositor
Resolution (Å)	78.35 – 2.20 19.59 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.1 (78.35-2.20) 97.3 (19.59-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.77 (at 2.21Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.229 , 0.283 0.234 , 0.284	Depositor DCC
R_{free} test set	2812 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	17.9	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.4	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	0.90	EDS
Total number of atoms	8200	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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

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	0.78	0/2037	0.87	1/2773 (0.0%)
1	B	0.79	0/1983	0.87	3/2705 (0.1%)
1	C	0.79	1/2012 (0.0%)	0.90	5/2741 (0.2%)
1	D	0.80	1/1905 (0.1%)	0.91	4/2601 (0.2%)
All	All	0.79	2/7937 (0.0%)	0.89	13/10820 (0.1%)

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	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	174	ASP	CB-CG	-6.63	1.37	1.51
1	D	174	ASP	CB-CG	-5.83	1.39	1.51

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	174	ASP	CB-CG-OD2	-8.55	110.61	118.30
1	C	144	ASP	CB-CG-OD1	6.98	124.58	118.30
1	D	179	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	D	179	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	B	81	VAL	CB-CA-C	5.50	121.86	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	245	GLY	Peptide

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	1996	0	1913	18	0
1	B	1942	0	1855	13	0
1	C	1971	0	1898	14	0
1	D	1867	0	1773	13	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	107	0	0	1	0
3	B	95	0	0	1	0
3	C	98	0	0	0	0
3	D	104	0	0	0	0
All	All	8200	0	7439	52	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.

The worst 5 of 52 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:12:GLN:HE22	1:D:12:GLN:HE22	1.32	0.76
1:C:245:GLY:O	1:C:248:GLN:HB2	1.92	0.70
1:B:216:LEU:HD22	1:B:221:GLY:HA3	1.79	0.65
1:A:10:LEU:HD13	1:A:52:THR:HG21	1.83	0.61
1:A:169:LYS:HG3	1:B:160:THR:HG22	1.83	0.60

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	256/275 (93%)	248 (97%)	8 (3%)	0	100	100
1	B	254/275 (92%)	248 (98%)	6 (2%)	0	100	100
1	C	252/275 (92%)	238 (94%)	12 (5%)	2 (1%)	19	19
1	D	243/275 (88%)	237 (98%)	4 (2%)	2 (1%)	19	19
All	All	1005/1100 (91%)	971 (97%)	30 (3%)	4 (0%)	34	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	246	LEU
1	D	24	GLN
1	C	245	GLY
1	D	162	PRO

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	206/232 (89%)	194 (94%)	12 (6%)	20	23
1	B	198/232 (85%)	185 (93%)	13 (7%)	16	19
1	C	205/232 (88%)	199 (97%)	6 (3%)	42	54
1	D	190/232 (82%)	179 (94%)	11 (6%)	20	23
All	All	799/928 (86%)	757 (95%)	42 (5%)	22	27

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	171	ILE
1	D	164	LEU
1	C	216	LEU
1	D	115	VAL
1	D	174	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	24	GLN
1	C	268	GLN
1	C	155	ASN
1	D	8	GLN
1	B	12	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)

4 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	$\#\|Z\| > 2$
2	PO4	C	301	-	4,4,4	0.58	0	6,6,6	1.38	1 (16%)
2	PO4	B	301	-	4,4,4	1.15	0	6,6,6	0.83	0
2	PO4	A	301	-	4,4,4	1.17	0	6,6,6	0.91	0
2	PO4	D	301	-	4,4,4	1.04	0	6,6,6	1.12	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	301	PO4	O2-P-O1	-2.38	102.20	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	262/275 (95%)	-0.17	2 (0%)	86	85	13, 26, 49, 67	0
1	B	258/275 (93%)	-0.09	4 (1%)	72	70	13, 26, 49, 67	0
1	C	258/275 (93%)	-0.08	5 (1%)	66	65	13, 29, 49, 67	0
1	D	249/275 (90%)	-0.18	2 (0%)	86	85	13, 25, 49, 62	0
All	All	1027/1100 (93%)	-0.13	13 (1%)	77	75	13, 26, 49, 67	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	26	LEU	4.4
1	C	50	PHE	2.7
1	A	67	GLY	2.7
1	B	2	ALA	2.6
1	C	27	THR	2.5

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	PO4	C	301	5/5	0.98	0.07	15,16,17,18	0
2	PO4	D	301	5/5	0.98	0.08	15,16,17,17	0
2	PO4	A	301	5/5	0.99	0.07	19,19,22,22	0
2	PO4	B	301	5/5	0.99	0.07	18,19,20,22	0

6.5 Other polymers (i)

There are no such residues in this entry.