wwPDB X-ray Structure Validation Summary Report (i)

Jan 7, 2024 – 10:29 am GMT

PDB ID	:	5O6G
Title	:	Structures and dynamics of mesophilic variants from the homing endonuclease I-DmoI
Authors	:	Molina, R.; Marcaida, M.J.
Deposited on	:	2017-06-06
Resolution	:	2.75 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 (1)) were used in the production of this report:

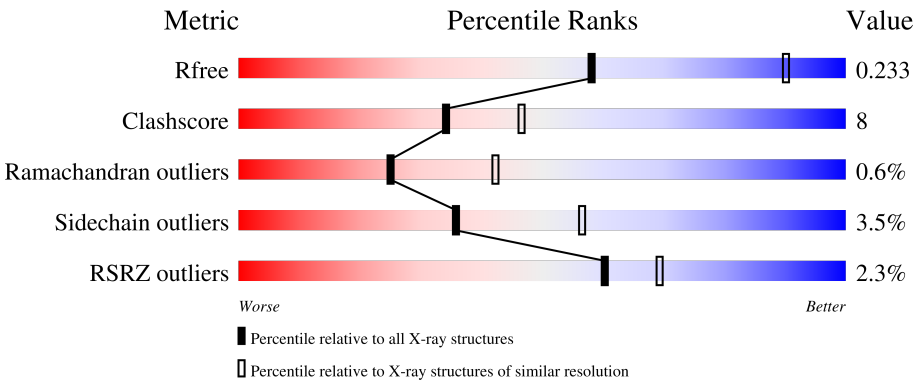
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	200	4% 68% 24% • 6%
1	D	200	2% 68% 20% • 11%
1	G	200	2% 67% 19% • 11%
2	B	25	52% 44% •
2	E	25	84% 16%

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Mol	Chain	Length	Quality of chain
2	H	25	44% 52% •
3	C	25	64% 36%
3	F	25	72% 28%
3	I	25	60% 36% •

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7676 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 Homing endonuclease I-DmoI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	188	1566	1012	284	267	3	0	3	0
1	D	178	1497	967	273	254	3	0	3	0
1	G	178	1497	967	273	254	3	0	3	0

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P21505
A	1	ALA	-	expression tag	UNP P21505
A	52	PHE	ILE	conflict	UNP P21505
A	95	GLN	LEU	conflict	UNP P21505
A	189	ALA	-	expression tag	UNP P21505
A	190	ALA	-	expression tag	UNP P21505
A	191	ALA	-	expression tag	UNP P21505
A	192	LEU	-	expression tag	UNP P21505
A	193	GLU	-	expression tag	UNP P21505
A	194	HIS	-	expression tag	UNP P21505
A	195	HIS	-	expression tag	UNP P21505
A	196	HIS	-	expression tag	UNP P21505
A	197	HIS	-	expression tag	UNP P21505
A	198	HIS	-	expression tag	UNP P21505
A	199	HIS	-	expression tag	UNP P21505
D	0	MET	-	initiating methionine	UNP P21505
D	1	ALA	-	expression tag	UNP P21505
D	52	PHE	ILE	conflict	UNP P21505
D	95	GLN	LEU	conflict	UNP P21505
D	189	ALA	-	expression tag	UNP P21505
D	190	ALA	-	expression tag	UNP P21505
D	191	ALA	-	expression tag	UNP P21505
D	192	LEU	-	expression tag	UNP P21505

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Chain	Residue	Modelled	Actual	Comment	Reference
D	193	GLU	-	expression tag	UNP P21505
D	194	HIS	-	expression tag	UNP P21505
D	195	HIS	-	expression tag	UNP P21505
D	196	HIS	-	expression tag	UNP P21505
D	197	HIS	-	expression tag	UNP P21505
D	198	HIS	-	expression tag	UNP P21505
D	199	HIS	-	expression tag	UNP P21505
G	0	MET	-	initiating methionine	UNP P21505
G	1	ALA	-	expression tag	UNP P21505
G	52	PHE	ILE	conflict	UNP P21505
G	95	GLN	LEU	conflict	UNP P21505
G	189	ALA	-	expression tag	UNP P21505
G	190	ALA	-	expression tag	UNP P21505
G	191	ALA	-	expression tag	UNP P21505
G	192	LEU	-	expression tag	UNP P21505
G	193	GLU	-	expression tag	UNP P21505
G	194	HIS	-	expression tag	UNP P21505
G	195	HIS	-	expression tag	UNP P21505
G	196	HIS	-	expression tag	UNP P21505
G	197	HIS	-	expression tag	UNP P21505
G	198	HIS	-	expression tag	UNP P21505
G	199	HIS	-	expression tag	UNP P21505

- Molecule 2 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	B	25	511	242	94	151	24	0	0	0
2	E	25	511	242	94	151	24	0	0	0
2	H	25	511	242	94	151	24	0	0	0

- Molecule 3 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	C	25	508	240	99	145	24	0	0	0
3	F	25	508	240	99	145	24	0	0	0
3	I	25	508	240	99	145	24	0	0	0

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Mn 2 2	0	0
4	D	2	Total Mn 2 2	0	0
4	G	2	Total Mn 2 2	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	1	Total Cl 1 1	1	0

- Molecule 6 is water.

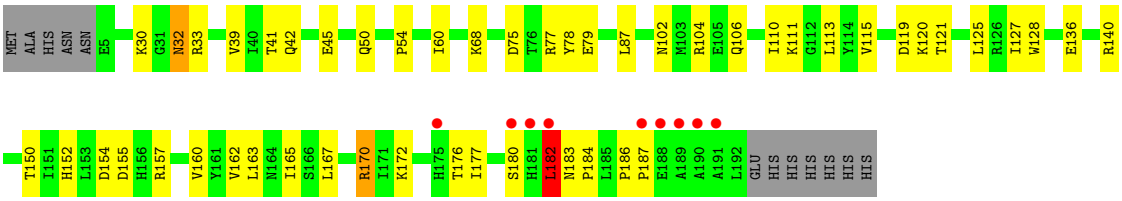
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	5	Total O 5 5	0	0
6	B	1	Total O 1 1	0	0
6	C	6	Total O 6 6	0	0
6	D	10	Total O 10 10	0	0
6	E	5	Total O 5 5	0	0
6	F	6	Total O 6 6	0	0
6	G	11	Total O 11 11	0	0
6	H	4	Total O 4 4	0	0
6	I	4	Total O 4 4	0	0

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.

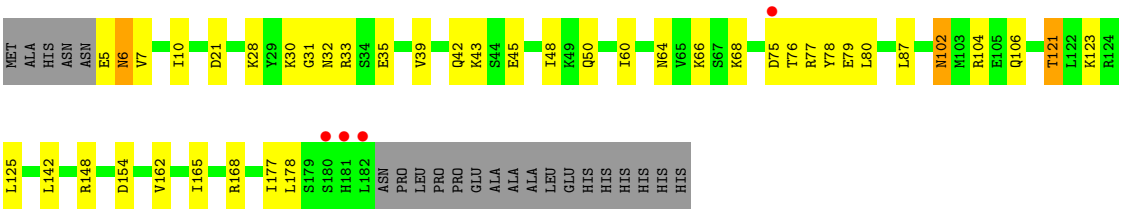
• Molecule 1: Homing endonuclease I-DmoI

Chain A:



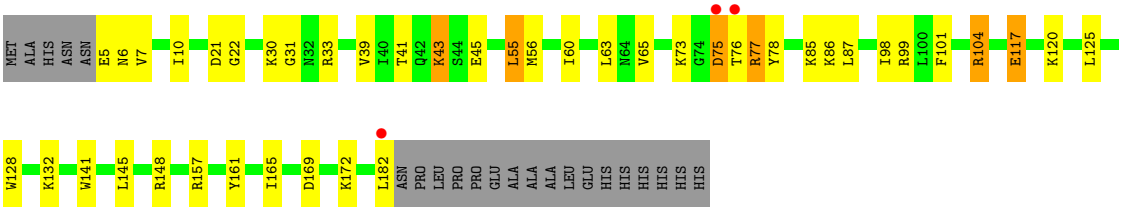
• Molecule 1: Homing endonuclease I-DmoI

Chain D:



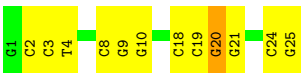
• Molecule 1: Homing endonuclease I-DmoI

Chain G:



• Molecule 2: DNA (25-MER)

Chain B:



- Molecule 2: DNA (25-MER)

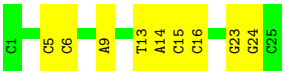
Chain E:

- Molecule 2: DNA (25-MER)

Chain H:

- Molecule 3: DNA (25-MER)

Chain C:

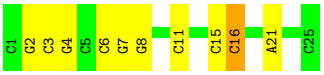


- Molecule 3: DNA (25-MER)

Chain F:

- Molecule 3: DNA (25-MER)

Chain I:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	107.28Å 70.50Å 107.15Å 90.00° 119.89° 90.00°	Depositor
Resolution (Å)	56.18 – 2.75 56.18 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.5 (56.18-2.75) 91.9 (56.18-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.73 (at 2.77Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.177 , 0.232 0.179 , 0.233	Depositor DCC
R_{free} test set	1995 reflections (5.62%)	wwPDB-VP
Wilson B-factor (Å^2)	49.9	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 51.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.029 for l,k,-h-l 0.029 for -h-l,k,h 0.025 for -h-l,-k,l 0.023 for h,-k,-h-l 0.026 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7676	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 3.61% 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: CL, MN

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	0.44	0/1605	0.65	1/2160 (0.0%)
1	D	0.44	0/1533	0.61	0/2058
1	G	0.46	0/1533	0.63	1/2058 (0.0%)
2	B	0.94	0/572	1.05	2/882 (0.2%)
2	E	0.95	0/572	1.06	2/882 (0.2%)
2	H	1.00	1/572 (0.2%)	1.07	1/882 (0.1%)
3	C	0.96	1/570 (0.2%)	1.01	1/877 (0.1%)
3	F	1.01	1/570 (0.2%)	1.06	3/877 (0.3%)
3	I	1.00	2/570 (0.4%)	1.02	2/877 (0.2%)
All	All	0.72	5/8097 (0.1%)	0.85	13/11553 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	15	DC	C3'-O3'	7.07	1.53	1.44
3	I	15	DC	C3'-O3'	5.91	1.51	1.44
3	C	15	DC	C3'-O3'	5.67	1.51	1.44
2	H	4	DT	O3'-P	-5.55	1.54	1.61
3	I	21	DA	O3'-P	-5.01	1.55	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	9	DA	O4'-C1'-N9	7.14	113.00	108.00
2	B	20	DG	O4'-C1'-N9	6.41	112.49	108.00
3	F	18	DG	O4'-C1'-N9	6.26	112.38	108.00
2	E	15	DG	OP1-P-OP2	-5.92	110.72	119.60
2	B	18	DC	O4'-C4'-C3'	-5.82	102.17	104.50

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	1566	0	1644	38	0
1	D	1497	0	1574	29	0
1	G	1497	0	1574	31	0
2	B	511	0	282	9	0
2	E	511	0	282	2	0
2	H	511	0	282	10	0
3	C	508	0	279	5	0
3	F	508	0	279	3	0
3	I	508	0	279	5	0
4	A	2	0	0	0	0
4	D	2	0	0	0	0
4	G	2	0	0	0	0
5	G	1	0	0	0	0
6	A	5	0	0	2	0
6	B	1	0	0	0	0
6	C	6	0	0	0	0
6	D	10	0	0	2	0
6	E	5	0	0	1	0
6	F	6	0	0	0	0
6	G	11	0	0	2	0
6	H	4	0	0	0	0
6	I	4	0	0	1	0
All	All	7676	0	6475	118	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 8.

The worst 5 of 118 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:G:10:ILE:HD13	1:G:55:LEU:HD23	1.48	0.95
1:G:30:LYS:NZ	2:H:20:DG:OP2	2.03	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:LYS:NZ	2:E:13:DA:OP2	2.07	0.88
1:G:10:ILE:HG23	1:G:55:LEU:HD22	1.61	0.83
1:D:30:LYS:O	1:D:33:ARG:NH1	2.13	0.81

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	189/200 (94%)	173 (92%)	16 (8%)	0	100	100
1	D	179/200 (90%)	167 (93%)	11 (6%)	1 (1%)	25	42
1	G	179/200 (90%)	170 (95%)	7 (4%)	2 (1%)	14	25
All	All	547/600 (91%)	510 (93%)	34 (6%)	3 (0%)	25	47

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	6	ASN
1	D	6	ASN
1	G	75	ASP

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	171/179 (96%)	167 (98%)	4 (2%)	50	69
1	D	164/179 (92%)	159 (97%)	5 (3%)	41	61
1	G	164/179 (92%)	156 (95%)	8 (5%)	25	43
All	All	499/537 (93%)	482 (97%)	17 (3%)	36	58

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	117	GLU
1	G	172	LYS
1	D	102	ASN
1	D	121	THR
1	G	43	LYS

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

Mol	Chain	Res	Type
1	A	6	ASN
1	D	102	ASN
1	D	106	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)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	188/200 (94%)	0.40	9 (4%)	30	36	28, 49, 86, 101	0
1	D	178/200 (89%)	0.25	4 (2%)	62	70	29, 45, 67, 120	0
1	G	178/200 (89%)	0.32	3 (1%)	70	78	33, 50, 72, 91	0
2	B	25/25 (100%)	-0.33	0	100	100	38, 57, 69, 75	0
2	E	25/25 (100%)	-0.33	0	100	100	40, 52, 64, 67	0
2	H	25/25 (100%)	-0.57	0	100	100	35, 55, 65, 68	0
3	C	25/25 (100%)	-0.32	0	100	100	38, 53, 81, 83	0
3	F	25/25 (100%)	-0.44	0	100	100	37, 53, 74, 77	0
3	I	25/25 (100%)	-0.26	0	100	100	40, 53, 74, 76	0
All	All	694/750 (92%)	0.17	16 (2%)	60	69	28, 49, 75, 120	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	182	LEU	5.6
1	A	181	HIS	5.2
1	A	188	GLU	5.1
1	G	75	ASP	4.7
1	A	190	ALA	4.5

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)

LIGAND-RSR INFOmissingINFO

6.5 Other polymers (i)

There are no such residues in this entry.