



# Full wwPDB X-ray Structure Validation Report i

Feb 26, 2014 – 06:01 PM GMT

PDB ID : 1DL3  
Title : CRYSTAL STRUCTURE OF MUTUALLY GENERATED MONOMERS OF  
DIMERIC PHOSPHORIBOSYLANTRANILATEISOMERASE FROM  
THERMOTOGA MARITIMA  
Authors : Thoma, R.; Hennig, M.; Sterner, R.; Kirschner, K.  
Deposited on : 1999-12-08  
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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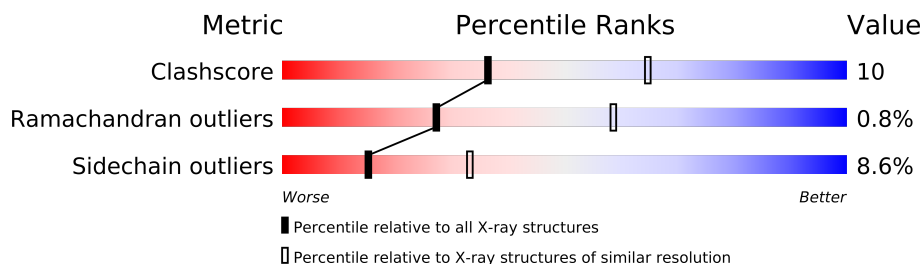
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	203	
1	B	203	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3128 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PROTEIN (PHOSPHORIBOSYLANTRANILATEISOMERASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	191	Total	C	N	O	S	0	0	0
			1529	980	263	281	5			
1	B	194	Total	C	N	O	S	0	0	0
			1557	999	267	286	5			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	TYR	ALA	MUTATION	UNP Q56320
A	?	-	PRO	DELETION	UNP Q56320
A	?	-	PHE	DELETION	UNP Q56320
A	55	GLU	PHE	MUTATION	UNP Q56320
A	101	TRP	ILE	MUTATION	UNP Q56320
B	1025	TYR	ALA	MUTATION	UNP Q56320
B	?	-	PRO	DELETION	UNP Q56320
B	?	-	PHE	DELETION	UNP Q56320
B	1055	GLU	PHE	MUTATION	UNP Q56320
B	1101	TRP	ILE	MUTATION	UNP Q56320

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	17	Total	O	0	0
			17	17		

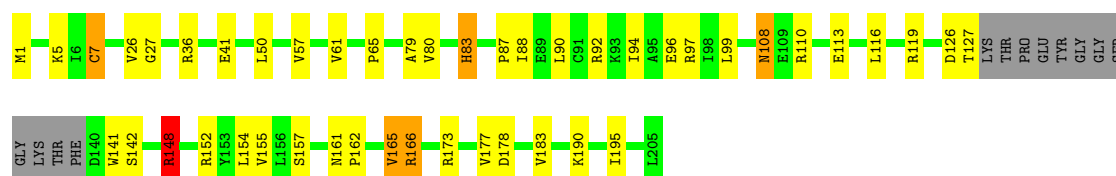
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

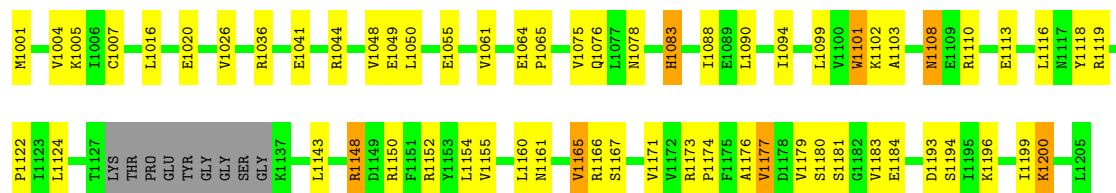
#### • Molecule 1: PROTEIN (PHOSPHORIBOSYLANTRANILATEISOMERASE)

Chain A: 



#### • Molecule 1: PROTEIN (PHOSPHORIBOSYLANTRANILATEISOMERASE)

Chain B: 



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.68Å 94.65Å 46.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.2 (20.00-2.70)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.175 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3128	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.40	0/1559	0.64	0/2108
1	B	0.42	0/1588	0.66	0/2145
All	All	0.41	0/3147	0.65	0/4253

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1529	0	1547	28	0
1	B	1557	0	1573	36	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
3	A	15	0	0	0	0
3	B	17	0	0	1	0
All	All	3128	0	3120	64	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

All (64) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:88:ILE:HD12	1:A:88:ILE:H	1.56	0.69
1:A:26:VAL:HG21	1:A:50:LEU:HD13	1.74	0.69
1:A:166:ARG:HE	1:A:166:ARG:HA	1.59	0.68
1:B:1148:ARG:HH21	1:B:1174:PRO:HA	1.60	0.66
1:A:92:ARG:O	1:A:96:GLU:HG3	1.96	0.66
1:B:1016:LEU:O	1:B:1020:GLU:HG2	1.99	0.63
1:B:1116:LEU:O	1:B:1119:ARG:HG2	1.99	0.63
1:B:1148:ARG:NH2	1:B:1174:PRO:HA	2.17	0.60
1:B:1055:GLU:HA	1:B:1078:ASN:HD22	1.70	0.57
1:A:65:PRO:HB3	1:A:94:ILE:HD11	1.87	0.57
1:A:1:MET:CE	1:A:1:MET:HA	2.35	0.56
1:B:1088:ILE:HD12	1:B:1088:ILE:H	1.70	0.55
1:B:1180:SER:HB3	2:B:400:SO4:O4	2.07	0.55
1:B:1064:GLU:HB2	1:B:1065:PRO:HD2	1.88	0.55
1:A:108:ASN:HD21	1:A:110:ARG:HG2	1.71	0.54
1:A:5:LYS:NZ	1:A:7:CYS:SG	2.80	0.54
1:B:1026:VAL:HG21	1:B:1050:LEU:HD13	1.89	0.54
1:B:1044:ARG:O	1:B:1048:VAL:HG23	2.08	0.53
1:A:26:VAL:HG21	1:A:50:LEU:CD1	2.38	0.53
1:B:1005:LYS:NZ	1:B:1007:CYS:SG	2.81	0.53
1:A:97:ARG:NE	1:A:97:ARG:HA	2.24	0.52
1:B:1113:GLU:O	1:B:1116:LEU:HB2	2.10	0.51
1:A:183:VAL:HG23	1:A:190:LYS:HD2	1.91	0.51
1:A:113:GLU:HA	1:A:116:LEU:HD12	1.92	0.51
1:A:65:PRO:CB	1:A:94:ILE:HD11	2.40	0.51
1:B:1001:MET:CE	1:B:1001:MET:HA	2.40	0.51
1:A:161:ASN:O	1:A:165:VAL:HG22	2.10	0.51
1:B:1124:LEU:HD12	1:B:1155:VAL:HG11	1.93	0.50
1:B:1004:VAL:HG11	1:B:1199:ILE:HG12	1.93	0.49
1:B:1155:VAL:HG22	1:B:1176:ALA:HB3	1.94	0.49
1:B:1124:LEU:HD12	1:B:1155:VAL:CG1	2.43	0.48
1:B:1103:ALA:HA	1:B:1124:LEU:O	2.14	0.47
1:A:127:THR:HB	1:A:141:TRP:HZ3	1.78	0.47
1:B:1160:LEU:HD13	1:B:1177:VAL:HG22	1.97	0.46
1:A:190:LYS:HB3	1:A:195:ILE:HD11	1.98	0.46
1:A:116:LEU:O	1:A:119:ARG:HG2	2.16	0.46
1:A:61:VAL:HG22	1:A:83:HIS:HB3	1.97	0.45
1:B:1108:ASN:ND2	1:B:1110:ARG:HG2	2.31	0.45
1:B:1148:ARG:HD3	1:B:1148:ARG:C	2.38	0.44
1:A:108:ASN:ND2	1:A:110:ARG:HG2	2.31	0.44
1:B:1150:ARG:HG3	3:B:29:HOH:O	2.17	0.44
1:A:57:VAL:HG22	1:A:79:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:1181:SER:HA	1:B:1184:GLU:HG3	2.00	0.44
1:B:1075:VAL:O	1:B:1076:GLN:HB2	2.19	0.43
1:B:1183:VAL:HA	1:B:1194:SER:HB3	2.00	0.43
1:A:97:ARG:HA	1:A:97:ARG:HE	1.83	0.42
1:B:1196:LYS:O	1:B:1200:LYS:HB2	2.18	0.42
1:B:1161:ASN:O	1:B:1165:VAL:HG22	2.18	0.42
1:B:1065:PRO:HD3	1:B:1090:LEU:HD11	2.00	0.42
1:B:1179:VAL:HG22	1:B:1180:SER:N	2.35	0.42
1:B:1102:LYS:HG2	1:B:1118:TYR:CD1	2.55	0.42
1:B:1065:PRO:HB3	1:B:1094:ILE:HD11	2.02	0.41
1:A:87:PRO:HG2	1:A:90:LEU:HB2	2.01	0.41
1:B:1061:VAL:HG22	1:B:1083:HIS:HB3	2.03	0.41
1:A:161:ASN:HB2	1:A:162:PRO:CD	2.51	0.41
1:A:161:ASN:HB2	1:A:162:PRO:HD2	2.03	0.41
1:B:1101:TRP:CD1	1:B:1122:PRO:HB2	2.55	0.41
1:B:1116:LEU:HD23	1:B:1116:LEU:HA	1.91	0.41
1:B:1167:SER:O	1:B:1171:VAL:HG23	2.20	0.41
1:A:154:LEU:HD12	1:A:155:VAL:N	2.36	0.41
1:A:148:ARG:HD3	1:A:148:ARG:C	2.40	0.40
1:A:27:GLY:HA2	1:A:57:VAL:O	2.21	0.40
1:B:1148:ARG:CZ	1:B:1154:LEU:HD23	2.52	0.40
1:A:157:SER:HB2	1:A:178:ASP:HB3	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	187/203 (92%)	170 (91%)	15 (8%)	2 (1%)	21	49
1	B	190/203 (94%)	170 (90%)	19 (10%)	1 (0%)	38	70
All	All	377/406 (93%)	340 (90%)	34 (9%)	3 (1%)	27	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	ARG
1	A	152	ARG
1	B	1152	ARG

### 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	168/177 (95%)	154 (92%)	14 (8%)	16	35
1	B	171/177 (97%)	156 (91%)	15 (9%)	14	32
All	All	339/354 (96%)	310 (91%)	29 (9%)	15	33

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

Mol	Chain	Res	Type
1	A	7	CYS
1	A	36	ARG
1	A	41	GLU
1	A	80	VAL
1	A	83	HIS
1	A	99	LEU
1	A	108	ASN
1	A	126	ASP
1	A	142	SER
1	A	148	ARG
1	A	165	VAL
1	A	166	ARG
1	A	173	ARG
1	A	177	VAL
1	B	1036	ARG
1	B	1041	GLU
1	B	1049	GLU
1	B	1083	HIS
1	B	1099	LEU
1	B	1101	TRP
1	B	1108	ASN
1	B	1143	LEU
1	B	1148	ARG

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Mol	Chain	Res	Type
1	B	1165	VAL
1	B	1166	ARG
1	B	1173	ARG
1	B	1177	VAL
1	B	1193	ASP
1	B	1200	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	108	ASN
1	B	1062	ASN
1	B	1078	ASN
1	B	1108	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	SO4	A	300	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	B	400	-	4,4,4	0.33	0	6,6,6	0.14	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	SO4	A	300	-	-	0/0/0/0	0/0/0/0
2	SO4	B	400	-	-	0/0/0/0	0/0/0/0

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.

## 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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.