



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:06 AM GMT

PDB ID : 2VXX
Title : X-RAY STRUCTURE OF DPSA FROM THERMOSYNECHOCOCCUS
ELONGATUS
Authors : Franceschini, S.; Ilari, A.
Deposited on : 2008-07-14
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

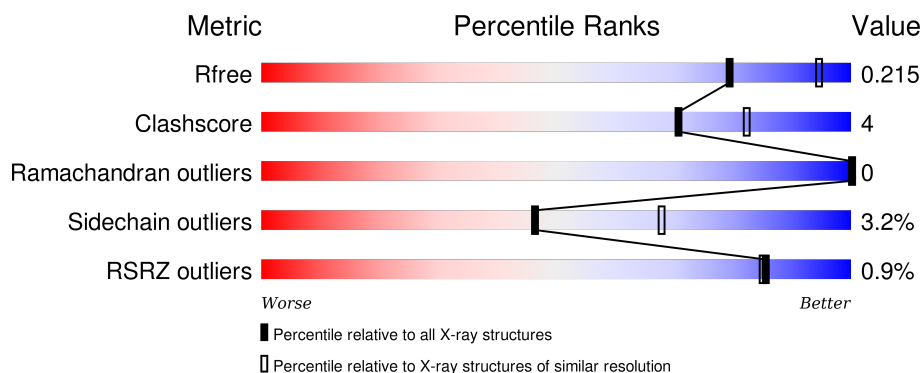
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	192	<div> <div></div> <div>83% 5% • 10%</div> </div>
1	B	192	<div> <div></div> <div>81% 9% • 10%</div> </div>
1	C	192	<div> <div></div> <div>80% 9% • 10%</div> </div>
1	D	192	<div> <div></div> <div>78% 10% • 10%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PG4	B	1177	-	-	-	X
5	PEG	C	1177	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6035 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 STARVATION INDUCED DNA BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	5	0
			1386	884	237	257	8			
1	B	173	Total	C	N	O	S	0	7	0
			1402	891	242	261	8			
1	C	173	Total	C	N	O	S	0	3	0
			1379	877	237	257	8			
1	D	172	Total	C	N	O	S	0	4	0
			1380	876	241	255	8			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Fe	0	0
			1	1		
3	C	1	Total	Fe	0	0
			1	1		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	103	Total 103	O 103	0	0
6	B	121	Total 121	O 121	0	0
6	C	106	Total 106	O 106	0	0
6	D	114	Total 114	O 114	0	0

- Molecule 1: STARVATION INDUCED DNA BINDING PROTEIN



MET	TMR	THR	S4	R8	V18	G32	Y44	F59	Y60	H63	D68	G69	E71	Q72	V73	Q74	M13	Q116	Q134	Q135	K157	E160	V176	LEU	LNS	VAL	LNS	LEU	ALA	ASP	GLY	ARG	GUJ	HIS	HIS	HIS	HIS	HIS	HIS	HIS
-----	-----	-----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

MET
THR
S4
A10
E13
G32
Q46
I47
Q48
Y60
P61
Y70
Q74
E107
G110
N113
Q116
E125
Q135
E140
R161
T165
V176
LEU
LYS
VAL
LYS
LEU
ALA
ASP
GLY
ARG
GLU
HIS
HIS
HIS
HIS
HIS

GLU	HIS	HIS	HIS	HIS	HIS	HIS
MET	TIR	TIR	SER	AS	L20	G32
						Q41
						Y44
						L45
						Q46
						P59
						Y60
						H63
						Y70
						H76
						Y90
						Q96
						E107
						M113
						C114
						R115
						Q116
						L117
						L118
						Q135
						E140
						L155
						E159
						E160
						R161
						L169
						V176
						LEU
						LYS
						VAL
						LYS
						LEU
						ALA
						ASP
						GLY

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	174.50Å 174.50Å 174.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	123.09 – 2.40 43.63 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (123.09-2.40) 99.9 (43.63-2.40)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0043	Depositor
R, R_{free}	0.165 , 0.216 0.165 , 0.215	Depositor DCC
R_{free} test set	1738 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.3	EDS
Estimated twinning fraction	0.026 for -l,-k,-h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34678 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6035	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, PEG, PG4, FE

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	0.39	0/1431	0.49	0/1939
1	B	0.40	0/1452	0.51	0/1965
1	C	0.40	0/1418	0.51	0/1923
1	D	0.40	0/1421	0.50	0/1924
All	All	0.40	0/5722	0.50	0/7751

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

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	1386	0	1351	13	0
1	B	1402	0	1372	11	0
1	C	1379	0	1335	14	0
1	D	1380	0	1345	19	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
4	B	13	0	18	2	0
5	B	7	0	10	0	0
5	C	7	0	10	0	0
5	D	7	0	10	0	0
6	A	103	0	0	0	0
6	B	121	0	0	2	0
6	C	106	0	0	1	0
6	D	114	0	0	3	0
All	All	6035	0	5451	49	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.

The worst 5 of 49 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:C:46:GLN:HE22	1:C:107:GLU:H	1.30	0.78
1:D:76:HIS:HE1	1:D:161:ARG:HH22	1.36	0.70
1:A:113:ASN:ND2	1:A:116[A]:GLN:H	1.93	0.66
1:A:113:ASN:ND2	1:A:116[B]:GLN:H	1.93	0.66
1:B:113:ASN:ND2	1:B:116:GLN:H	1.94	0.65

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	175/192 (91%)	174 (99%)	1 (1%)	0	100	100
1	B	178/192 (93%)	176 (99%)	2 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	174/192 (91%)	171 (98%)	3 (2%)	0	100	100
1	D	174/192 (91%)	171 (98%)	3 (2%)	0	100	100
All	All	701/768 (91%)	692 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	144/158 (91%)	141 (98%)	3 (2%)	61	80
1	B	147/158 (93%)	141 (96%)	6 (4%)	37	57
1	C	143/158 (90%)	139 (97%)	4 (3%)	51	72
1	D	143/158 (90%)	137 (96%)	6 (4%)	36	56
All	All	577/632 (91%)	558 (97%)	19 (3%)	46	66

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	113	ASN
1	C	60[B]	TYR
1	D	70	TYR
1	B	70	TYR
1	D	96	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	113	ASN
1	C	74	GLN
1	D	134	GLN
1	C	46	GLN
1	C	48	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	$\# Z > 2$
4	PG4	B	1177	-	12,12,12	0.54	0	11,11,11	0.37	0
5	PEG	B	1178	-	6,6,6	0.42	0	5,5,5	0.34	0
5	PEG	C	1177	-	6,6,6	0.45	0	5,5,5	0.37	0
5	PEG	D	1177	-	6,6,6	0.44	0	5,5,5	0.35	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
4	PG4	B	1177	-	-	0/10/10/10	0/0/0/0
5	PEG	B	1178	-	-	0/4/4/4	0/0/0/0
5	PEG	C	1177	-	-	0/4/4/4	0/0/0/0
5	PEG	D	1177	-	-	0/4/4/4	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1177	PG4	2	0

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 [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	172/192 (89%)	-0.43	2 (1%) 81 81	17, 22, 32, 44	0
1	B	173/192 (90%)	-0.70	1 (0%) 90 90	18, 22, 31, 42	0
1	C	173/192 (90%)	-0.41	2 (1%) 81 81	17, 22, 33, 43	0
1	D	172/192 (89%)	-0.41	1 (0%) 90 90	17, 22, 30, 41	0
All	All	690/768 (89%)	-0.49	6 (0%) 85 85	17, 22, 31, 44	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	176	VAL	7.1
1	D	176	VAL	4.8
1	A	176	VAL	4.7
1	B	176	VAL	4.3
1	C	4	SER	3.3

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	PG4	B	1177	13/13	0.78	0.27	5.01	59,60,60,61	0
5	PEG	C	1177	7/7	0.73	0.39	3.47	69,69,70,70	0
5	PEG	D	1177	7/7	0.85	0.28	1.39	46,46,47,47	0
2	ZN	C	201	1/1	0.99	0.07	-1.76	32,32,32,32	0
2	ZN	B	201	1/1	0.99	0.04	-3.25	41,41,41,41	0
3	FE	C	203	1/1	0.98	0.12	-	49,49,49,49	0
2	ZN	A	201	1/1	1.00	0.04	-	25,25,25,25	0
2	ZN	B	202	1/1	1.00	0.01	-	26,26,26,26	0
2	ZN	A	202	1/1	0.98	0.09	-	45,45,45,45	0
2	ZN	D	202	1/1	1.00	0.05	-	22,22,22,22	0
5	PEG	B	1178	7/7	0.89	0.15	-	52,53,54,55	0
2	ZN	D	201	1/1	0.99	0.09	-	32,32,32,32	0
2	ZN	C	202	1/1	1.00	0.01	-	24,24,24,24	0
3	FE	B	203	1/1	0.99	0.09	-	24,24,24,24	1

6.5 Other polymers

There are no such residues in this entry.