wwPDB X-ray Structure Validation Summary Report (i)

Nov 7, 2023 – 05:33 PM JST

PDB ID	:	7CNX
Title	:	Crystal structure of Apo PSD from E. coli (2.63 A)
Authors	:	Kim, J.; Cho, G.
Deposited on	:	2020-08-03
Resolution	:	2.63 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:

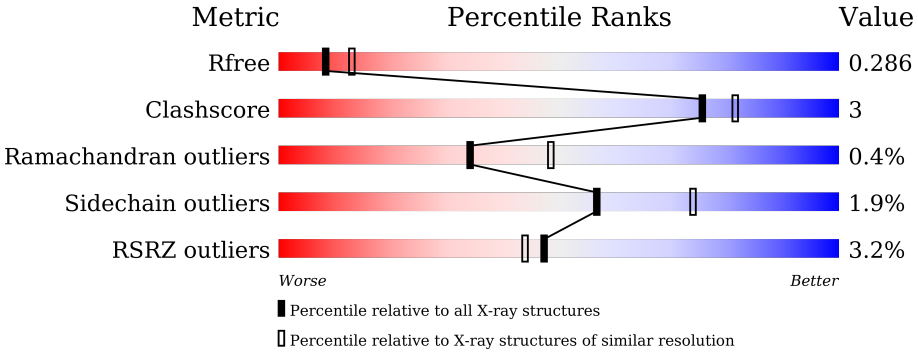
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.63 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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	253	4% 90% 7% •
1	C	253	4% 86% 9% 5%
1	E	253	% 91% 8% •
1	G	253	4% 89% 7% • •
2	B	42	83% 10% 7%
2	D	42	2% 52% 29% 19%

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Mol	Chain	Length	Quality of chain
2	F	42	81% 10% 10%
2	H	42	79% 17% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8453 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 Phosphatidylserine decarboxylase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1871	1205	316	341	9	0	0	0
1	C	240	1830	1180	316	325	9	0	1	0
1	E	249	1887	1213	322	343	9	0	0	0
1	G	244	1811	1161	310	331	9	0	0	0

- Molecule 2 is a protein called Phosphatidylserine decarboxylase alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	39	268	170	46	52	0	0	0
2	D	34	236	153	37	46	0	0	0
2	F	38	264	170	45	49	0	0	0
2	H	40	272	174	49	49	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	254	PYR	SER	modified residue	UNP A0A6D2XQZ0
B	288	GLY	-	expression tag	UNP A0A6D2XQZ0
B	289	HIS	-	expression tag	UNP A0A6D2XQZ0
B	290	HIS	-	expression tag	UNP A0A6D2XQZ0
B	291	HIS	-	expression tag	UNP A0A6D2XQZ0
B	292	HIS	-	expression tag	UNP A0A6D2XQZ0
B	293	HIS	-	expression tag	UNP A0A6D2XQZ0
B	294	HIS	-	expression tag	UNP A0A6D2XQZ0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	295	GLY	-	expression tag	UNP A0A6D2XQZ0
D	254	PYR	SER	modified residue	UNP A0A6D2XQZ0
D	288	GLY	-	expression tag	UNP A0A6D2XQZ0
D	289	HIS	-	expression tag	UNP A0A6D2XQZ0
D	290	HIS	-	expression tag	UNP A0A6D2XQZ0
D	291	HIS	-	expression tag	UNP A0A6D2XQZ0
D	292	HIS	-	expression tag	UNP A0A6D2XQZ0
D	293	HIS	-	expression tag	UNP A0A6D2XQZ0
D	294	HIS	-	expression tag	UNP A0A6D2XQZ0
D	295	GLY	-	expression tag	UNP A0A6D2XQZ0
F	254	PYR	SER	modified residue	UNP A0A6D2XQZ0
F	288	GLY	-	expression tag	UNP A0A6D2XQZ0
F	289	HIS	-	expression tag	UNP A0A6D2XQZ0
F	290	HIS	-	expression tag	UNP A0A6D2XQZ0
F	291	HIS	-	expression tag	UNP A0A6D2XQZ0
F	292	HIS	-	expression tag	UNP A0A6D2XQZ0
F	293	HIS	-	expression tag	UNP A0A6D2XQZ0
F	294	HIS	-	expression tag	UNP A0A6D2XQZ0
F	295	GLY	-	expression tag	UNP A0A6D2XQZ0
H	254	PYR	SER	modified residue	UNP A0A6D2XQZ0
H	288	GLY	-	expression tag	UNP A0A6D2XQZ0
H	289	HIS	-	expression tag	UNP A0A6D2XQZ0
H	290	HIS	-	expression tag	UNP A0A6D2XQZ0
H	291	HIS	-	expression tag	UNP A0A6D2XQZ0
H	292	HIS	-	expression tag	UNP A0A6D2XQZ0
H	293	HIS	-	expression tag	UNP A0A6D2XQZ0
H	294	HIS	-	expression tag	UNP A0A6D2XQZ0
H	295	GLY	-	expression tag	UNP A0A6D2XQZ0

- Molecule 3 is water.

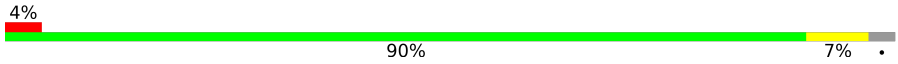
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	2	2	2	0	0
			Total	O		
3	B	1	1	1	0	0
			Total	O		
3	C	3	3	3	0	0
			Total	O		
3	E	6	6	6	0	0
			Total	O		
3	G	2	2	2	0	0

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.

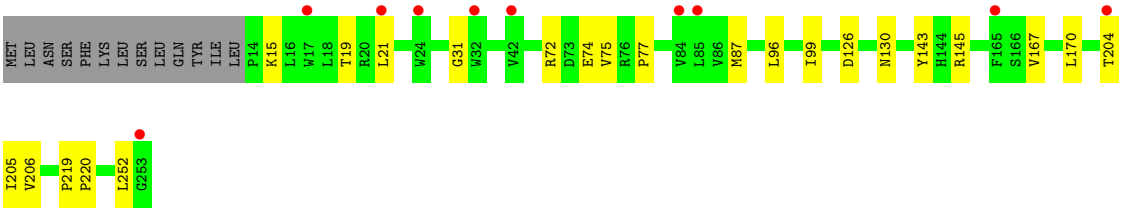
• Molecule 1: Phosphatidylserine decarboxylase beta chain

Chain A:



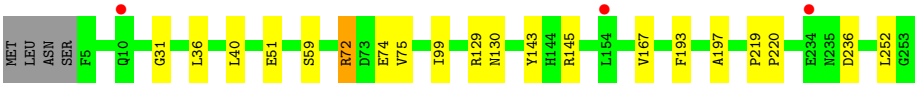
• Molecule 1: Phosphatidylserine decarboxylase beta chain

Chain C:



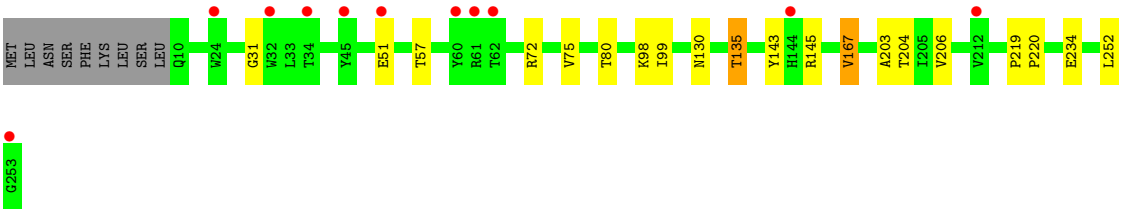
• Molecule 1: Phosphatidylserine decarboxylase beta chain

Chain E:



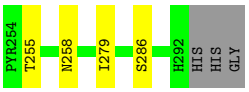
• Molecule 1: Phosphatidylserine decarboxylase beta chain

Chain G:



• Molecule 2: Phosphatidylserine decarboxylase alpha chain

Chain B:

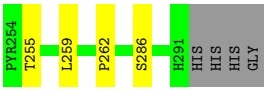


• Molecule 2: Phosphatidylserine decarboxylase alpha chain

Chain D:

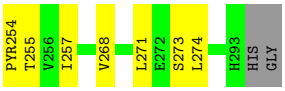
• Molecule 2: Phosphatidylserine decarboxylase alpha chain

Chain F:



• Molecule 2: Phosphatidylserine decarboxylase alpha chain

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	79.90Å 101.85Å 170.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.78 – 2.63 48.78 – 2.63	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.78-2.63) 100.0 (48.78-2.63)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.24 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.231 , 0.288 0.232 , 0.286	Depositor DCC
R_{free} test set	2056 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	65.3	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 47.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8453	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: PYR

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	0.67	0/1919	0.80	0/2622
1	C	0.67	0/1880	0.81	1/2567 (0.0%)
1	E	0.68	0/1934	0.81	0/2640
1	G	0.67	0/1858	0.78	0/2541
2	B	0.72	0/267	0.89	0/366
2	D	0.71	0/233	0.84	0/320
2	F	0.73	0/263	0.88	0/361
2	H	0.76	0/272	0.86	0/373
All	All	0.68	0/8626	0.81	1/11790 (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
2	D	0	1
2	H	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	126	ASP	CB-CA-C	5.64	121.69	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	254	PYR	Peptide
2	H	254	PYR	Mainchain

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	1871	0	1773	10	0
1	C	1830	0	1752	14	0
1	E	1887	0	1787	11	0
1	G	1811	0	1658	11	0
2	B	268	0	248	4	0
2	D	236	0	242	7	0
2	F	264	0	258	4	0
2	H	272	0	254	4	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	E	6	0	0	0	0
3	G	2	0	0	0	0
All	All	8453	0	7972	50	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 50 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:15:LYS:O	1:C:19:THR:HG23	1.64	0.97
1:C:19:THR:HG22	1:C:205:ILE:H	1.39	0.85
1:E:51:GLU:HG2	1:E:75:VAL:HG21	1.72	0.70
1:C:167:VAL:HG11	2:D:255:THR:OG1	1.96	0.66
1:A:51:GLU:HG2	1:A:75:VAL:HG21	1.78	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	244/253 (96%)	233 (96%)	10 (4%)	1 (0%)	34	48
1	C	239/253 (94%)	228 (95%)	10 (4%)	1 (0%)	34	48
1	E	247/253 (98%)	237 (96%)	9 (4%)	1 (0%)	34	48
1	G	242/253 (96%)	231 (96%)	10 (4%)	1 (0%)	34	48
2	B	37/42 (88%)	34 (92%)	3 (8%)	0	100	100
2	D	32/42 (76%)	30 (94%)	2 (6%)	0	100	100
2	F	36/42 (86%)	34 (94%)	2 (6%)	0	100	100
2	H	38/42 (90%)	34 (90%)	4 (10%)	0	100	100
All	All	1115/1180 (94%)	1061 (95%)	50 (4%)	4 (0%)	34	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	GLY
1	E	31	GLY
1	G	31	GLY
1	C	31	GLY

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	185/216 (86%)	182 (98%)	3 (2%)	62	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	180/216 (83%)	178 (99%)	2 (1%)	73	85
1	E	185/216 (86%)	181 (98%)	4 (2%)	52	70
1	G	169/216 (78%)	163 (96%)	6 (4%)	35	52
2	B	26/35 (74%)	26 (100%)	0	100	100
2	D	26/35 (74%)	25 (96%)	1 (4%)	33	50
2	F	27/35 (77%)	27 (100%)	0	100	100
2	H	26/35 (74%)	26 (100%)	0	100	100
All	All	824/1004 (82%)	808 (98%)	16 (2%)	57	74

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	167	VAL
1	G	135	THR
1	E	74	GLU
1	G	98	LYS
1	E	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	289	HIS
2	H	291	HIS

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)

There are no ligands in this entry.

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	246/253 (97%)	0.04	11 (4%)	33	30	48, 63, 93, 107	0
1	C	240/253 (94%)	0.24	10 (4%)	36	33	51, 74, 96, 112	0
1	E	249/253 (98%)	-0.04	3 (1%)	79	77	46, 62, 92, 134	0
1	G	244/253 (96%)	0.15	11 (4%)	33	30	53, 76, 106, 122	0
2	B	38/42 (90%)	-0.22	0	100	100	50, 58, 81, 105	0
2	D	33/42 (78%)	0.23	1 (3%)	50	46	53, 76, 88, 99	0
2	F	37/42 (88%)	-0.39	0	100	100	50, 59, 82, 91	0
2	H	39/42 (92%)	0.18	0	100	100	60, 76, 99, 106	0
All	All	1126/1180 (95%)	0.08	36 (3%)	47	44	46, 69, 99, 134	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	253	GLY	4.1
1	C	165	PHE	4.0
1	G	34	THR	3.9
1	G	32	TRP	3.8
1	E	234	GLU	3.8

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.