



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 08:25 AM GMT

PDB ID : 1B9X
Title : STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATED
ION-REGULATED INTERACTION WITH TRANSDUCIN
Authors : Gaudet, R.; Sigler, P.B.
Deposited on : 1999-02-16
Resolution : 3.00 Å (reported)

This is a wwPDB 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/ValidationPDFNotes.html>

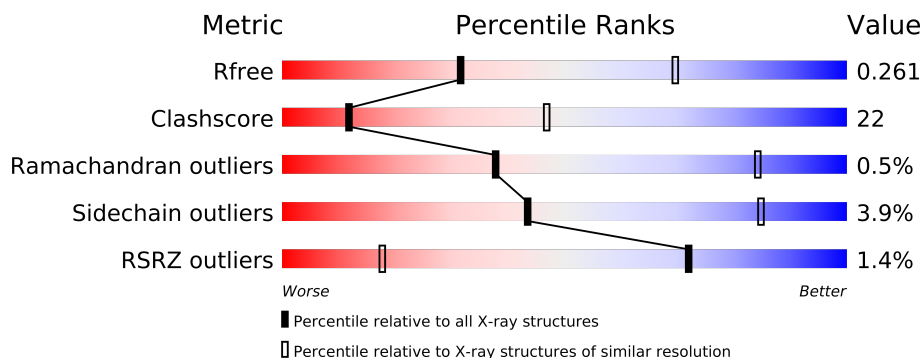
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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 3.00 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}	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	340	
2	B	68	
3	C	246	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4538 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 (TRANSDUCIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2616	1613	469	512	22			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	LEU	VAL	CONFLICT	UNP P62871

- Molecule 2 is a protein called PROTEIN (TRANSDUCIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	68	Total	C	N	O	S	0	0	0
			559	351	90	113	5			

- Molecule 3 is a protein called PROTEIN (PHOSDUCIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	169	Total	C	N	O	S	0	0	0
			1339	848	224	259	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	GLU	SER	SEE REMARK 999	UNP P02698

- Molecule 4 is GADOLINIUM ATOM (three-letter code: Gd) (formula: Gd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Gd	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Gd 2	0	0
4	C	2	Total 2	Gd 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total 8	O 8	0	0
5	B	5	Total 5	O 5	0	0
5	C	5	Total 5	O 5	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.04Å 89.33Å 100.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 50.13 – 3.02	Depositor EDS
% Data completeness (in resolution range)	90.4 (50.00-3.00) 98.3 (50.13-3.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 3.01Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.217 , 0.261 0.225 , 0.261	Depositor DCC
R_{free} test set	1308 reflections (10.61%)	DCC
Wilson B-factor (Å ²)	54.3	Xtriage
Anisotropy	0.725	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 13631 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4538	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.42	0/2663	0.72	0/3608
2	B	0.38	0/565	0.64	0/753
3	C	0.45	0/1364	0.63	0/1835
All	All	0.42	0/4592	0.69	0/6196

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	2616	0	2524	129	0
2	B	559	0	570	37	0
3	C	1339	0	1293	44	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
5	A	8	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4538	0	4387	193	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 22.

The worst 5 of 193 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:217:MET:HE1	2:B:524:LYS:HZ2	1.10	1.11
1:A:78:LYS:HE3	1:A:92:ALA:HB1	1.37	1.05
1:A:217:MET:HE1	2:B:524:LYS:NZ	1.72	1.03
1:A:266:HIS:CE1	1:A:268:ASN:HD22	1.77	1.02
3:C:18:THR:HB	3:C:27:ASN:HD22	1.25	1.00

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	338/340 (99%)	315 (93%)	23 (7%)	0	100	100
2	B	66/68 (97%)	64 (97%)	1 (2%)	1 (2%)	15	58
3	C	165/246 (67%)	153 (93%)	10 (6%)	2 (1%)	19	64
All	All	569/654 (87%)	532 (94%)	34 (6%)	3 (0%)	38	84

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	229	GLU
3	C	178	GLY
2	B	566	GLU

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	283/283 (100%)	273 (96%)	10 (4%)	48	87
2	B	66/66 (100%)	63 (96%)	3 (4%)	38	81
3	C	143/218 (66%)	137 (96%)	6 (4%)	40	83
All	All	492/567 (87%)	473 (96%)	19 (4%)	43	85

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

Mol	Chain	Res	Type
1	A	236	PRO
2	B	505	ASN
3	C	179	ASP
1	A	234	PHE
3	C	200	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	505	ASN
3	C	16	GLN
3	C	152	ASN
1	A	268	ASN
3	C	139	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 ⓘ

Of 6 ligands modelled in this entry, 6 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.

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 ⓘ

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	340/340 (100%)	-0.04	4 (1%) 75 20	18, 48, 90, 101	0
2	B	68/68 (100%)	0.19	3 (4%) 33 7	30, 61, 101, 101	0
3	C	169/246 (68%)	0.13	1 (0%) 86 32	23, 61, 101, 101	0
All	All	577/654 (88%)	0.04	8 (1%) 72 18	18, 52, 101, 101	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	501	MET	4.7
2	B	568	LYS	4.4
1	A	1	MET	3.4
1	A	132	ASN	2.9
3	C	87	GLU	2.8

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	GD	A	342	1/1	0.15	1.09	101,101,101,101	0
4	GD	B	102	1/1	0.18	-0.38	64,64,64,64	0
4	GD	C	247	1/1	0.17	-0.47	56,56,56,56	0
4	GD	A	341	1/1	0.21	-0.76	42,42,42,42	0
4	GD	B	104	1/1	0.16	-0.88	65,65,65,65	0
4	GD	C	248	1/1	0.13	-3.77	79,79,79,79	0

6.5 Other polymers ⓘ

There are no such residues in this entry.