



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 10:45 am BST

PDB ID : 2IXO
Title : CRYSTAL STRUCTURE OF THE PP2A PHOSPHATASE ACTIVATOR Ypa1 PTPA1
Authors : Leulliot, N.; Vicentini, G.; Jordens, J.; Quevillon-Cheruel, S.; Schiltz, M.; Barford, D.; Van Tilbeurgh, H.; Goris, J.
Deposited on : 2006-07-09
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

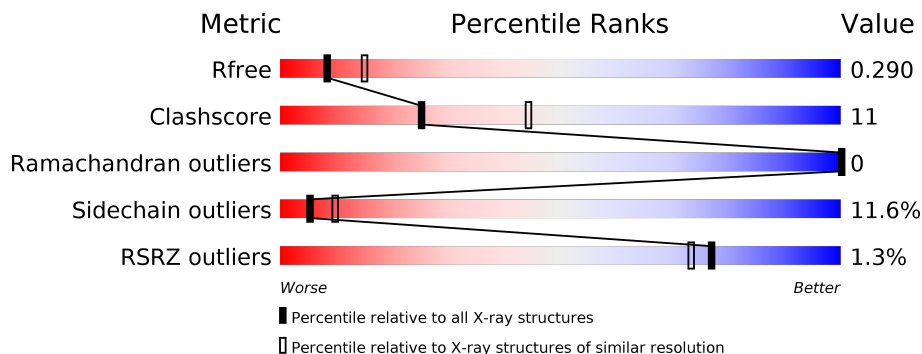
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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 $\leq 5\%$. 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	323	 71% 20% • 5%
1	B	323	 67% 25% • •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5071 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 SERINE/THREONINE-PROTEIN PHOSPHATASE 2A ACTIVATOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	307	2505	1629	417	446	13	0	0	0
1	B	312	2544	1651	428	452	13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	168	HIS	MET	conflict	UNP P40454
A	296	GLU	LEU	conflict	UNP P40454
B	168	HIS	MET	conflict	UNP P40454
B	296	GLU	LEU	conflict	UNP P40454

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	11	Total	O	0	0
			11	11		
2	B	11	Total	O	0	0
			11	11		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.08Å 94.18Å 139.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 33.13 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.5 (30.00-2.60) 95.5 (33.13-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.211 , 0.291 0.211 , 0.290	Depositor DCC
R_{free} test set	1103 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5071	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.88	0/2583	0.85	0/3511
1	B	0.86	0/2625	0.90	5/3571 (0.1%)
All	All	0.87	0/5208	0.87	5/7082 (0.1%)

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
1	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	191	TYR	C-N-CA	-5.82	107.16	121.70
1	B	141	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	B	160	ASP	CB-CG-OD1	5.39	123.15	118.30
1	B	175	LEU	CA-CB-CG	5.14	127.12	115.30
1	B	175	LEU	CB-CG-CD2	-5.07	102.38	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	89	GLY	Peptide

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	2505	0	2440	44	0
1	B	2544	0	2482	63	0
2	A	11	0	0	0	0
2	B	11	0	0	3	0
All	All	5071	0	4922	107	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 11.

All (107) 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:A:21:PHE:H	1:A:25:THR:HG21	1.27	0.98
1:A:185:ARG:NH2	1:A:250:GLN:HE21	1.63	0.95
1:A:75:ASP:OD1	1:A:179:LYS:HE2	1.70	0.92
1:A:185:ARG:HH21	1:A:250:GLN:HE21	1.21	0.87
1:B:62:SER:H	1:B:68:ASN:HD21	1.21	0.87
1:A:87:LEU:O	1:A:88:PRO:HA	1.78	0.83
1:B:19:ARG:HG2	1:B:314:TRP:CG	2.15	0.82
1:A:145:GLY:H	1:A:148:HIS:HD2	1.25	0.82
1:B:71:MET:CE	1:B:179:LYS:HG2	2.10	0.82
1:B:71:MET:HE1	1:B:179:LYS:HG2	1.65	0.78
1:B:145:GLY:H	1:B:148:HIS:HD2	1.29	0.77
1:B:19:ARG:HB2	1:B:307:PHE:CD1	2.20	0.76
1:A:21:PHE:H	1:A:25:THR:CG2	2.01	0.74
1:B:49:ILE:HG12	1:B:173:VAL:HG22	1.70	0.74
1:B:19:ARG:HG2	1:B:314:TRP:CD2	2.22	0.73
1:B:110:PRO:HG3	1:B:129:GLN:OE1	1.89	0.72
1:B:313:PRO:HB2	1:B:315:VAL:HG12	1.72	0.72
1:B:79:HIS:HB3	2:B:2003:HOH:O	1.88	0.72
1:B:49:ILE:HD12	1:B:218:GLN:HG2	1.72	0.71
1:B:141:ARG:HG3	1:B:141:ARG:HH11	1.54	0.71
1:B:272:ASP:O	1:B:276:THR:HB	1.92	0.69
1:A:62:SER:H	1:A:68:ASN:HD21	1.41	0.68
1:A:75:ASP:OD1	1:A:179:LYS:CE	2.43	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:ARG:HH21	1:A:250:GLN:NE2	1.91	0.66
1:B:104:LYS:O	1:B:108:ARG:HG2	1.96	0.66
1:A:316:ASN:HD22	1:A:317:ILE:N	1.93	0.66
1:A:316:ASN:HD22	1:A:317:ILE:H	1.42	0.65
1:A:262:PRO:HG2	1:A:265:GLU:OE1	1.97	0.64
1:B:33:LEU:HD12	1:B:313:PRO:HD2	1.78	0.64
1:B:246:ASN:HD22	1:B:249:CYS:H	1.46	0.63
1:B:62:SER:N	1:B:68:ASN:HD21	1.93	0.62
1:B:71:MET:HE3	1:B:179:LYS:HG2	1.82	0.62
1:B:33:LEU:HD11	1:B:37:ARG:CZ	2.30	0.61
1:B:299:PHE:CE1	1:B:303:GLN:HG3	2.38	0.59
1:B:33:LEU:HD12	1:B:313:PRO:CD	2.33	0.58
1:A:62:SER:HB3	1:A:67:VAL:HG22	1.85	0.57
1:A:228:LEU:HD21	1:A:238:LEU:HD22	1.86	0.57
1:B:184:MET:O	1:B:188:ILE:HG13	2.05	0.56
1:A:279:ARG:HG2	1:A:279:ARG:HH11	1.70	0.56
1:A:64:ILE:HB	1:A:67:VAL:HG13	1.88	0.55
1:B:71:MET:HE1	1:B:179:LYS:CG	2.37	0.55
1:B:64:ILE:HB	1:B:67:VAL:HG13	1.88	0.55
1:A:87:LEU:O	1:A:88:PRO:CA	2.53	0.53
1:B:145:GLY:H	1:B:148:HIS:CD2	2.18	0.53
1:A:22:ASP:H	1:A:25:THR:HG22	1.72	0.53
1:A:22:ASP:O	1:A:25:THR:HG22	2.07	0.53
1:A:53:SER:HB3	1:A:222:LEU:HD21	1.90	0.53
1:A:299:PHE:O	1:A:303:GLN:HB2	2.09	0.53
1:A:20:ILE:HA	1:A:25:THR:HG23	1.90	0.52
1:B:62:SER:HB3	1:B:67:VAL:HG22	1.91	0.52
1:A:316:ASN:O	1:A:317:ILE:HB	2.09	0.52
1:A:87:LEU:C	1:A:88:PRO:N	2.63	0.52
1:A:266:HIS:HD2	1:A:267:SER:OG	1.93	0.52
1:B:141:ARG:CG	1:B:141:ARG:HH11	2.20	0.52
1:A:174:PHE:O	1:A:178:ASN:HB2	2.11	0.51
1:B:119:SER:HA	1:B:122:HIS:CE1	2.45	0.51
1:A:67:VAL:O	1:A:71:MET:HG2	2.11	0.51
1:A:251:GLY:O	1:A:255:ILE:HG13	2.11	0.51
1:B:295:VAL:O	1:B:302:VAL:HG13	2.11	0.51
1:A:158:ALA:HB1	1:A:311:PHE:CD2	2.46	0.50
1:B:239:VAL:CG1	1:B:253:ASN:HB2	2.41	0.50
1:A:220:GLN:HB2	1:A:281:SER:HA	1.93	0.50
1:A:145:GLY:H	1:A:148:HIS:CD2	2.17	0.50
1:B:18:LYS:NZ	1:B:303:GLN:HE21	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ILE:HG12	1:A:39:LYS:HE2	1.93	0.49
1:B:239:VAL:HG12	1:B:253:ASN:HB2	1.93	0.49
1:B:18:LYS:HG3	1:B:19:ARG:N	2.27	0.49
1:A:121:TYR:O	1:A:124:VAL:HB	2.12	0.48
1:B:6:VAL:HG11	1:B:13:PHE:HZ	1.79	0.48
1:B:93:TYR:O	1:B:192:THR:HB	2.13	0.48
1:B:19:ARG:HB2	1:B:307:PHE:HD1	1.75	0.48
1:A:313:PRO:HB2	1:A:315:VAL:HG13	1.97	0.47
1:A:144:TYR:CE1	1:A:148:HIS:HB2	2.48	0.47
1:B:29:PHE:CE1	1:B:35:ILE:HB	2.50	0.47
1:A:94:GLY:HA2	1:A:192:THR:O	2.16	0.46
1:B:77:LEU:CD2	1:B:105:LEU:HD13	2.46	0.46
1:B:144:TYR:O	1:B:207:HIS:HD2	1.99	0.46
1:B:18:LYS:HG2	1:B:21:PHE:CZ	2.51	0.45
1:B:264:GLU:HG3	1:B:271:TYR:CD2	2.52	0.45
1:B:105:LEU:HD11	1:B:109:LEU:HD13	1.97	0.45
1:A:191:TYR:O	1:A:192:THR:C	2.55	0.45
1:B:18:LYS:HE3	1:B:21:PHE:CE2	2.51	0.45
1:B:246:ASN:ND2	1:B:249:CYS:H	2.11	0.45
1:B:22:ASP:O	1:B:299:PHE:CD1	2.70	0.44
1:A:135:SER:HB3	1:A:152:PHE:HB2	1.99	0.44
1:B:303:GLN:HB3	1:B:304:HIS:CD2	2.52	0.44
1:B:151:SER:HB3	2:B:2005:HOH:O	2.17	0.43
1:B:277:VAL:HA	1:B:278:PRO:HD3	1.67	0.43
1:A:20:ILE:HA	1:A:25:THR:CG2	2.49	0.43
1:B:208:PHE:HB3	1:B:211:VAL:HG22	2.00	0.43
1:B:212:TYR:HB3	1:B:248:TYR:CE1	2.54	0.43
1:B:96:LEU:HD22	1:B:142:LEU:HD21	2.01	0.42
1:B:149:GLU:CD	1:B:210:LEU:HB2	2.39	0.42
1:A:272:ASP:O	1:A:276:THR:HB	2.19	0.42
1:A:210:LEU:O	1:A:211:VAL:C	2.56	0.42
1:B:111:GLN:O	1:B:115:GLU:HG3	2.21	0.41
1:B:130:TYR:CD2	1:B:130:TYR:C	2.93	0.41
1:B:186:ARG:HG2	2:B:2008:HOH:O	2.20	0.41
1:B:77:LEU:HA	1:B:77:LEU:HD23	1.83	0.41
1:B:71:MET:HB3	1:B:71:MET:HE2	1.93	0.41
1:A:77:LEU:HD22	1:A:105:LEU:HG	2.02	0.41
1:B:144:TYR:CE1	1:B:148:HIS:HB2	2.55	0.41
1:B:109:LEU:N	1:B:110:PRO:CD	2.83	0.41
1:B:316:ASN:OD1	1:B:317:ILE:N	2.53	0.41
1:B:75:ASP:OD1	1:B:179:LYS:NZ	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ILE:HG23	1:A:259:LYS:HD2	2.03	0.40
1:B:41:HIS:O	1:B:42:LEU:C	2.56	0.40

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	299/323 (93%)	284 (95%)	15 (5%)	0	100	100
1	B	308/323 (95%)	290 (94%)	18 (6%)	0	100	100
All	All	607/646 (94%)	574 (95%)	33 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	275/289 (95%)	244 (89%)	31 (11%)	6	10
1	B	279/289 (96%)	246 (88%)	33 (12%)	5	9
All	All	554/578 (96%)	490 (88%)	64 (12%)	5	10

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	17	VAL
1	A	22	ASP
1	A	25	THR
1	A	27	LEU
1	A	82	ASP
1	A	93	TYR
1	A	105	LEU
1	A	138	SER
1	A	151	SER
1	A	164	MET
1	A	173	VAL
1	A	204	LEU
1	A	211	VAL
1	A	214	LEU
1	A	222	LEU
1	A	225	GLN
1	A	233	ILE
1	A	241	GLU
1	A	245	THR
1	A	258	VAL
1	A	265	GLU
1	A	267	SER
1	A	275	VAL
1	A	276	THR
1	A	279	ARG
1	A	295	VAL
1	A	296	GLU
1	A	309	THR
1	A	315	VAL
1	A	316	ASN
1	B	5	ARG
1	B	17	VAL
1	B	18	LYS
1	B	19	ARG
1	B	22	ASP
1	B	25	THR
1	B	28	ASP
1	B	49	ILE
1	B	60	THR
1	B	63	SER
1	B	67	VAL
1	B	71	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	93	TYR
1	B	120	GLU
1	B	122	HIS
1	B	124	VAL
1	B	138	SER
1	B	141	ARG
1	B	142	LEU
1	B	151	SER
1	B	164	MET
1	B	168	HIS
1	B	210	LEU
1	B	211	VAL
1	B	214	LEU
1	B	245	THR
1	B	258	VAL
1	B	265	GLU
1	B	272	ASP
1	B	276	THR
1	B	289	LYS
1	B	296	GLU
1	B	309	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	148	HIS
1	A	168	HIS
1	A	207	HIS
1	A	209	HIS
1	A	250	GLN
1	A	253	ASN
1	A	266	HIS
1	A	316	ASN
1	B	43	HIS
1	B	68	ASN
1	B	148	HIS
1	B	207	HIS
1	B	246	ASN
1	B	266	HIS
1	B	303	GLN
1	B	304	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 carbohydrates 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	87:LEU	C	88:PRO	N	2.63

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	307/323 (95%)	-0.39	3 (0%) 82 80	9, 24, 45, 60	0
1	B	312/323 (96%)	-0.31	5 (1%) 72 68	10, 26, 42, 51	0
All	All	619/646 (95%)	-0.35	8 (1%) 77 73	9, 25, 44, 60	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	198	SER	3.2
1	B	93	TYR	3.2
1	B	260	MET	3.0
1	A	10	HIS	2.8
1	B	265	GLU	2.6
1	A	7	ASP	2.6
1	B	79	HIS	2.5
1	A	265	GLU	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.