



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2FH7 / pdb_00002fh7
Title : Crystal structure of the phosphatase domains of human PTP SIGMA
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Deposited on : 2005-12-23
Resolution : 2.00 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

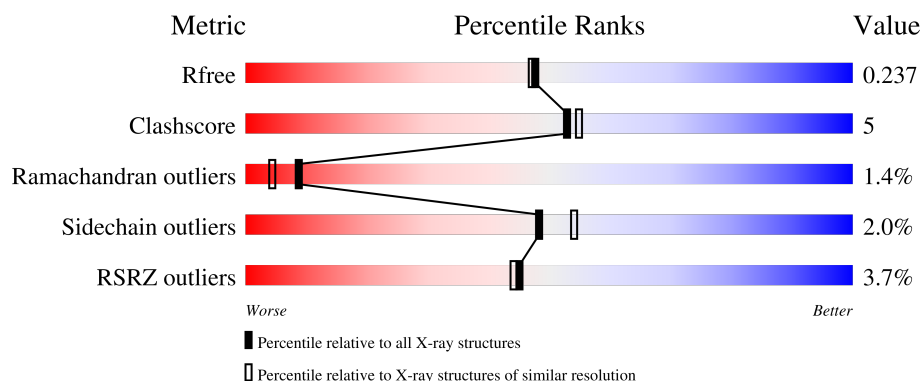
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

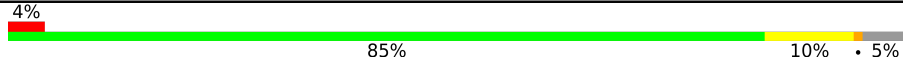
The reported resolution of this entry is 2.00 Å.

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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 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 $\leq 5\%$. 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	595	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5009 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 Receptor-type tyrosine-protein phosphatase S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	568	Total	C	N	O	S	0	8	0
			4648	2945	813	859	31			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1362	MET	-	cloning artifact	UNP Q13332
A	1363	SER	-	cloning artifact	UNP Q13332
A	1364	LEU	-	cloning artifact	UNP Q13332
A	1949	GLU	-	cloning artifact	UNP Q13332
A	1950	GLY	-	cloning artifact	UNP Q13332
A	1951	HIS	-	expression tag	UNP Q13332
A	1952	HIS	-	expression tag	UNP Q13332
A	1953	HIS	-	expression tag	UNP Q13332
A	1954	HIS	-	expression tag	UNP Q13332
A	1955	HIS	-	expression tag	UNP Q13332
A	1956	HIS	-	expression tag	UNP Q13332

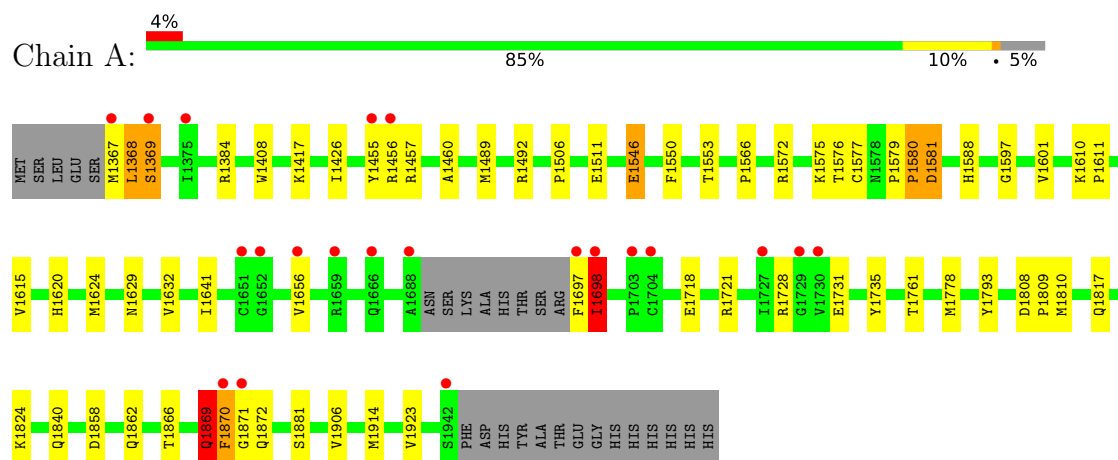
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	361	Total	O	0	0
			361	361		

3 Residue-property plots

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: Receptor-type tyrosine-protein phosphatase S



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	94.33Å 94.33Å 123.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.67 – 2.00 24.67 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.67-2.00) 99.9 (24.67-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.88 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.238 0.190 , 0.237	Depositor DCC
R_{free} test set	2103 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.051 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5009	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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	0.58	0/4761	0.79	7/6453 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1579	PRO	CA-C-N	6.51	127.98	119.84
1	A	1579	PRO	C-N-CA	6.51	127.98	119.84
1	A	1698	ILE	N-CA-C	5.79	115.97	110.53
1	A	1869	GLN	N-CA-C	5.20	119.95	111.37
1	A	1872	GLN	N-CA-C	5.06	117.44	110.35
1	A	1869	GLN	CA-C-N	5.03	130.75	121.70
1	A	1869	GLN	C-N-CA	5.03	130.75	121.70

There are no chirality outliers.

There are no planarity outliers.

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	4648	0	4516	46	0
2	A	361	0	0	5	0
All	All	5009	0	4516	46	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 5.

All (46) 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:1546:GLU:HG2	2:A:105:HOH:O	1.78	0.83
1:A:1367:MET:HA	1:A:1368:LEU:O	1.80	0.81
1:A:1870:PHE:CB	1:A:1871:GLY:HA2	2.12	0.79
1:A:1869:GLN:HG3	1:A:1870:PHE:HA	1.64	0.79
1:A:1601[A]:VAL:HG21	1:A:1641:ILE:HD13	1.66	0.75
1:A:1368:LEU:O	1:A:1369:SER:HB2	1.91	0.69
1:A:1492:ARG:HD3	2:A:92:HOH:O	1.98	0.63
1:A:1455:TYR:O	1:A:1457[A]:ARG:HD2	2.00	0.61
1:A:1550:PHE:HZ	1:A:1577:CYS:HB2	1.67	0.59
1:A:1457[B]:ARG:HB3	1:A:1460:ALA:HB2	1.85	0.58
1:A:1367:MET:HA	1:A:1368:LEU:C	2.30	0.56
1:A:1457[A]:ARG:HB3	1:A:1460:ALA:HB2	1.89	0.55
1:A:1601[A]:VAL:HG21	1:A:1641:ILE:CD1	2.37	0.54
1:A:1601[A]:VAL:HG12	1:A:1620:HIS:HD2	1.74	0.53
1:A:1368:LEU:O	1:A:1369:SER:CB	2.57	0.53
1:A:1550:PHE:CZ	1:A:1577:CYS:HB2	2.44	0.53
1:A:1572:ARG:O	1:A:1576:THR:HG23	2.08	0.53
1:A:1808:ASP:HB3	1:A:1810:MET:HE3	1.90	0.52
1:A:1810:MET:HG3	1:A:1824:LYS:HD3	1.90	0.51
1:A:1492:ARG:HD2	1:A:1553:THR:O	2.12	0.50
1:A:1870:PHE:CB	1:A:1871:GLY:CA	2.85	0.50
1:A:1597:GLY:O	1:A:1601[B]:VAL:HG23	2.12	0.50
1:A:1718:GLU:O	1:A:1721:ARG:HG2	2.13	0.48
1:A:1601[A]:VAL:HG13	1:A:1624:MET:SD	2.56	0.46
1:A:1809:PRO:O	1:A:1810:MET:HE2	2.17	0.45
1:A:1881:SER:HB3	2:A:179:HOH:O	2.16	0.45
1:A:1489:MET:HG3	1:A:1588:HIS:CE1	2.51	0.45
1:A:1808:ASP:CB	1:A:1810:MET:HE3	2.47	0.45
1:A:1858:ASP:O	1:A:1862:GLN:HG2	2.18	0.43
1:A:1869:GLN:CG	1:A:1870:PHE:HA	2.42	0.43
1:A:1721:ARG:HH21	1:A:1735:TYR:HA	1.84	0.43
1:A:1817:GLN:HE21	1:A:1817:GLN:HB3	1.65	0.43
1:A:1566:PRO:HA	1:A:1914:MET:HE1	2.00	0.43
1:A:1778:MET:HG2	1:A:1840:GLN:HG3	2.01	0.43
1:A:1697:PHE:HB3	1:A:1698:ILE:H	1.64	0.42
1:A:1417[A]:LYS:HD2	2:A:119:HOH:O	2.19	0.41
1:A:1580:PRO:HB2	1:A:1581[B]:ASP:H	1.71	0.41
1:A:1492:ARG:NH2	2:A:259:HOH:O	2.54	0.41
1:A:1506:PRO:HB3	1:A:1511:GLU:HB2	2.02	0.41
1:A:1408:TRP:HB3	1:A:1426:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1866:THR:O	1:A:1870:PHE:CB	2.68	0.41
1:A:1869:GLN:HG3	1:A:1870:PHE:CA	2.44	0.41
1:A:1869:GLN:N	1:A:1870:PHE:CB	2.84	0.41
1:A:1610:LYS:HB2	1:A:1611:PRO:HD3	2.02	0.41
1:A:1761:THR:HG23	1:A:1793:TYR:HB2	2.03	0.41
1:A:1455:TYR:CZ	1:A:1456:ARG:HD2	2.57	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	572/595 (96%)	542 (95%)	22 (4%)	8 (1%)	9 4

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1580	PRO
1	A	1368	LEU
1	A	1369	SER
1	A	1870	PHE
1	A	1728	ARG
1	A	1731	GLU
1	A	1632	VAL
1	A	1923	VAL

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	500/522 (96%)	487 (97%)	13 (3%)	40 44

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1384[A]	ARG
1	A	1384[B]	ARG
1	A	1546	GLU
1	A	1575	LYS
1	A	1581[A]	ASP
1	A	1581[B]	ASP
1	A	1615	VAL
1	A	1629	ASN
1	A	1656[A]	VAL
1	A	1656[B]	VAL
1	A	1698	ILE
1	A	1869	GLN
1	A	1906	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1404	GLN
1	A	1405	GLN
1	A	1436	GLN
1	A	1701	ASN
1	A	1817	GLN
1	A	1869	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 [i](#)

There are no oligosaccharides 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	568/595 (95%)	0.23	21 (3%) 45 44	8, 27, 46, 60	10 (1%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1367	MET	10.6
1	A	1651	CYS	6.6
1	A	1730	VAL	3.9
1	A	1698	ILE	3.8
1	A	1455	TYR	3.6
1	A	1729	GLY	3.5
1	A	1697	PHE	3.0
1	A	1369	SER	3.0
1	A	1870	PHE	3.0
1	A	1727	ILE	2.9
1	A	1703	PRO	2.9
1	A	1375	ILE	2.7
1	A	1652	GLY	2.5
1	A	1688	ALA	2.5
1	A	1456	ARG	2.3
1	A	1656[A]	VAL	2.2
1	A	1942	SER	2.2
1	A	1666	GLN	2.1
1	A	1704	CYS	2.1
1	A	1659	ARG	2.1
1	A	1871	GLY	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 oligosaccharides 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.