



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2GJT / pdb_00002gjt
Title : Crystal structure of the human receptor phosphatase PTPRO
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Deposited on : 2006-03-31
Resolution : 2.15 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

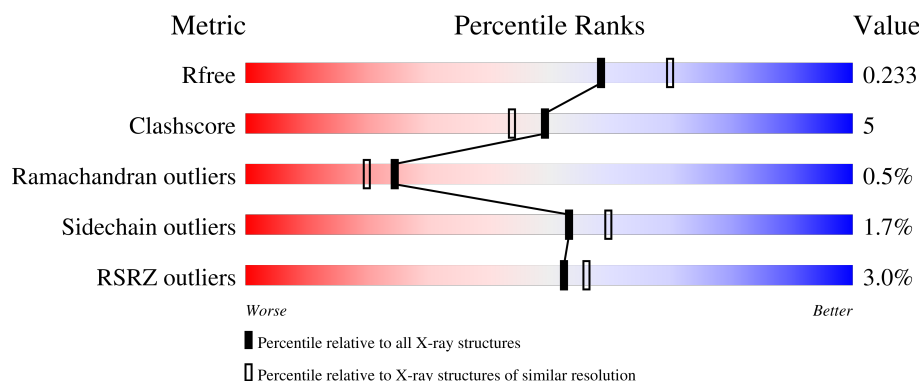
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	295	87% 12% .
1	B	295	4% 83% 10% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4827 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 PTPRO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	1	0
			2399	1527	403	447	22			
1	B	277	Total	C	N	O	S	0	2	0
			2209	1418	376	397	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	914	SER	-	cloning artifact	UNP Q16827
A	915	MET	-	cloning artifact	UNP Q16827
B	914	SER	-	cloning artifact	UNP Q16827
B	915	MET	-	cloning artifact	UNP Q16827

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	Cl	0	0
			5	5		
2	B	1	Total	Cl	0	0
			1	1		

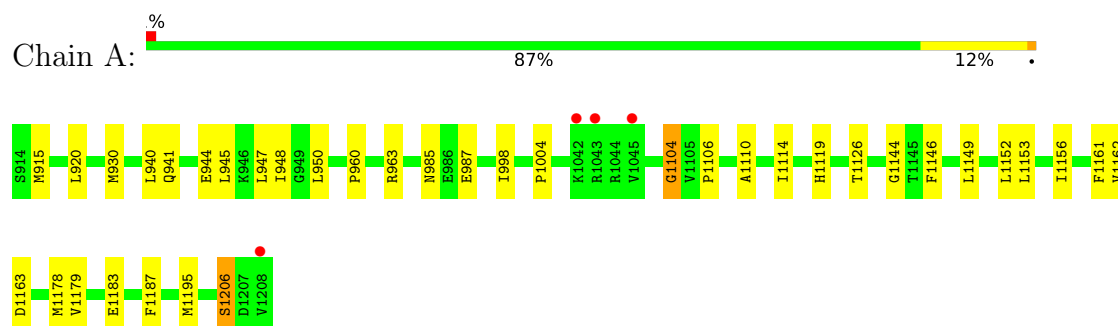
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	144	Total	O	0	3
			147	147		
3	B	66	Total	O	0	0
			66	66		

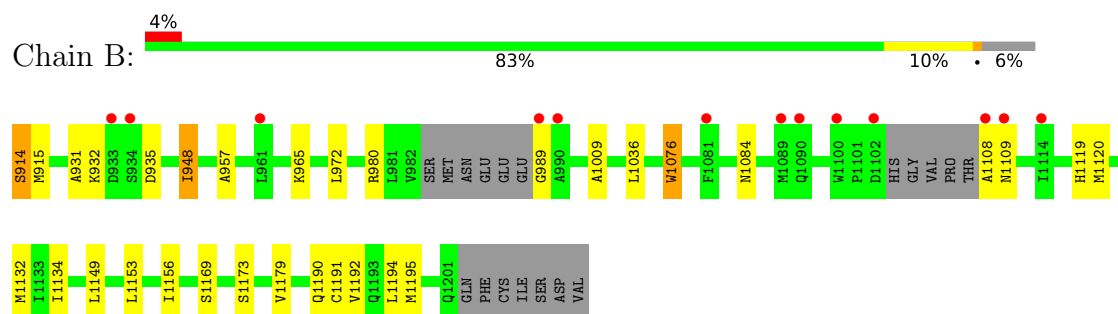
3 Residue-property plots

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 PTPRO



• Molecule 1: Receptor-type tyrosine-protein phosphatase PTPRO



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	131.06Å 131.06Å 77.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.91 – 2.15 42.91 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.91-2.15) 99.8 (42.91-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.179 , 0.234 0.181 , 0.233	Depositor DCC
R_{free} test set	2076 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.041 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4827	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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

5.1 Standard geometry

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

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	1.10	1/2462 (0.0%)	1.02	2/3334 (0.1%)
1	B	0.93	1/2271 (0.0%)	0.97	2/3081 (0.1%)
All	All	1.02	2/4733 (0.0%)	1.00	4/6415 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1206	SER	CB-OG	6.94	1.56	1.42
1	B	1009	ALA	CA-CB	-5.35	1.45	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1076	TRP	N-CA-C	5.59	117.03	108.42
1	B	1084	ASN	N-CA-C	5.36	117.40	108.99
1	A	998	ILE	CA-C-N	-5.24	114.32	119.92
1	A	998	ILE	C-N-CA	-5.24	114.32	119.92

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	932	LYS	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	2399	0	2281	26	0
1	B	2209	0	2063	24	0
2	A	5	0	0	0	0
2	B	1	0	0	0	0
3	A	147	0	0	2	0
3	B	66	0	0	1	0
All	All	4827	0	4344	48	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 (48) 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:B:1153:LEU:HA	1:B:1195:MET:HE1	1.43	0.98
1:B:1153:LEU:HA	1:B:1195:MET:CE	2.02	0.89
1:B:1108:ALA:CB	1:B:1109:ASN:HA	2.03	0.89
1:B:1108:ALA:HB3	1:B:1109:ASN:HA	1.52	0.88
1:A:1153:LEU:HA	1:A:1195:MET:CE	2.08	0.83
1:B:1108:ALA:HB1	1:B:1109:ASN:C	2.06	0.81
1:A:1153:LEU:HD23	1:A:1195:MET:HE3	1.61	0.80
1:B:1153:LEU:CA	1:B:1195:MET:HE1	2.12	0.79
1:B:1153:LEU:HD12	1:B:1195:MET:HE3	1.62	0.79
1:B:1108:ALA:CB	1:B:1109:ASN:CA	2.64	0.76
1:A:1153:LEU:HA	1:A:1195:MET:HE1	1.72	0.71
1:A:1153:LEU:HA	1:A:1195:MET:HE3	1.71	0.71
1:B:1108:ALA:HB1	1:B:1109:ASN:CA	2.30	0.60
1:A:1152:LEU:C	1:A:1195:MET:HE1	2.30	0.57
1:B:980[A]:ARG:NH1	3:B:70:HOH:O	2.41	0.54
1:A:1144:GLY:HA2	1:A:1178:MET:HE3	1.89	0.54
1:A:1104:GLY:O	1:A:1106:PRO:HD3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:PRO:HG3	1:B:1173:SER:HB3	1.90	0.53
1:B:1076:TRP:CD1	1:B:1120:MET:HE1	2.44	0.53
1:B:1153:LEU:N	1:B:1195:MET:HE1	2.23	0.52
1:B:1132:MET:HG2	1:B:1134:ILE:HD11	1.90	0.52
1:A:1152:LEU:O	1:A:1195:MET:HE1	2.10	0.52
1:A:1126:THR:HG22	3:A:135:HOH:O	2.09	0.52
1:B:1156:ILE:HD11	1:B:1192:VAL:HG13	1.93	0.51
1:A:1104:GLY:HA2	1:A:1183:GLU:OE2	2.11	0.50
1:A:1156:ILE:HD11	1:A:1162:VAL:HG11	1.92	0.50
1:A:945:LEU:HD23	1:A:948:ILE:HD12	1.93	0.50
1:B:1119[B]:HIS:CE1	1:B:1153:LEU:HD11	2.47	0.49
1:A:930:MET:HE1	1:A:941:GLN:CD	2.37	0.49
1:B:931:ALA:HA	1:B:935:ASP:OD1	2.14	0.48
1:A:1114:ILE:HD12	1:A:1187:PHE:CZ	2.49	0.48
1:A:941:GLN:O	1:A:944:GLU:HB2	2.14	0.47
1:A:1153:LEU:CA	1:A:1195:MET:HE1	2.43	0.47
1:B:965:LYS:NZ	1:B:989:GLY:O	2.48	0.47
1:A:1146:PHE:CD2	1:A:1146:PHE:C	2.92	0.46
1:B:957:ALA:HB1	1:B:972:LEU:HD22	1.99	0.45
1:B:1191:CYS:O	1:B:1195:MET:HG3	2.17	0.45
1:B:914:SER:HB2	1:B:1169:SER:OG	2.18	0.44
1:B:1190:GLN:O	1:B:1194:LEU:HD13	2.16	0.44
1:A:915:MET:HB2	1:A:1163:ASP:OD2	2.18	0.44
1:A:945:LEU:HA	1:A:948:ILE:HD12	1.99	0.43
1:A:1119:HIS:ND1	3:A:248:HOH:O	2.36	0.43
1:A:1110:ALA:O	1:A:1114:ILE:HG13	2.18	0.42
1:B:948:ILE:HD12	1:B:948:ILE:HG21	1.55	0.42
1:A:985:ASN:HB3	1:A:987:GLU:H	1.85	0.42
1:A:960:PRO:O	1:A:963:ARG:HG2	2.21	0.41
1:A:947:LEU:O	1:A:950:LEU:HG	2.21	0.40
1:A:1161:PHE:HZ	1:B:915:MET:HE2	1.85	0.40

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	294/295 (100%)	287 (98%)	5 (2%)	2 (1%)	18	13
1	B	273/295 (92%)	262 (96%)	10 (4%)	1 (0%)	30	26
All	All	567/590 (96%)	549 (97%)	15 (3%)	3 (0%)	24	20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1104	GLY
1	A	1179	VAL
1	B	1179	VAL

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	257/267 (96%)	253 (98%)	4 (2%)	55	61
1	B	222/267 (83%)	218 (98%)	4 (2%)	51	58
All	All	479/534 (90%)	471 (98%)	8 (2%)	53	60

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	920	LEU
1	A	940	LEU
1	A	1149	LEU
1	A	1206	SER
1	B	914	SER
1	B	948	ILE
1	B	1036	LEU
1	B	1149	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	916	ASN
1	A	919	GLN
1	A	941	GLN
1	A	1002	ASN
1	A	1019	ASN
1	A	1116	GLN
1	A	1201	GLN
1	B	1040	ASN
1	B	1073	GLN
1	B	1080	HIS
1	B	1084	ASN
1	B	1180	GLN
1	B	1190	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

No monomer is involved in short contacts.

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	295/295 (100%)	0.14	4 (1%) 73 77	20, 35, 52, 72	1 (0%)
1	B	277/295 (93%)	0.62	13 (4%) 36 41	21, 39, 59, 86	2 (0%)
All	All	572/590 (96%)	0.37	17 (2%) 52 56	20, 37, 57, 86	3 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1102	ASP	5.6
1	B	1114	ILE	4.4
1	B	933	ASP	4.0
1	B	1100	TRP	2.7
1	B	1108	ALA	2.6
1	B	961	LEU	2.6
1	A	1045	VAL	2.6
1	A	1208	VAL	2.4
1	B	1081	PHE	2.4
1	B	990	ALA	2.4
1	B	934	SER	2.4
1	B	989	GLY	2.3
1	B	1109	ASN	2.2
1	B	1089	MET	2.2
1	B	1090	GLN	2.0
1	A	1043	ARG	2.0
1	A	1042	LYS	2.0

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 [i](#)

There are no oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	A	302	1/1	0.81	0.24	72,72,72,72	0
2	CL	A	301	1/1	0.87	0.15	60,60,60,60	0
2	CL	B	304	1/1	0.88	0.18	67,67,67,67	0
2	CL	A	306	1/1	0.91	0.15	69,69,69,69	0
2	CL	A	305	1/1	0.92	0.15	69,69,69,69	0
2	CL	A	303	1/1	0.93	0.13	64,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.