Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:28 PM GMT

PDB ID	:	4S0G
Title	:	Crystal structure of PTPN3 (PTPH1) in complex with Eps15 pTyr849 P850V peptide
Authors	:	Chen, K.-E.; Meng, T.C.; Wang, A.H.-J.
Deposited on	:	2014-12-31
Resolution	:	1.72 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
http://wwpdb.org/validation/2016/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:

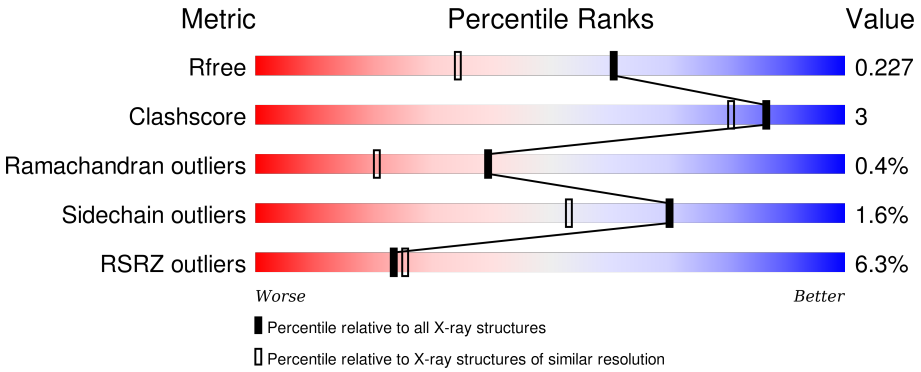
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 1.72 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}	91344	3998 (1.74-1.70)
Clashscore	102246	4425 (1.74-1.70)
Ramachandran outliers	100387	4360 (1.74-1.70)
Sidechain outliers	100360	4360 (1.74-1.70)
RSRZ outliers	91569	4010 (1.74-1.70)

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. 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	306	6%, 83%, 7%, •, 9%
2	B	9	67%, 33%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4707 atoms, of which 2272 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 Tyrosine-protein phosphatase non-receptor type 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	279	4480	1426	2233	381	422	18	74	5	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	604	MET	-	EXPRESSION TAG	UNP P26045
A	605	HIS	-	EXPRESSION TAG	UNP P26045
A	606	HIS	-	EXPRESSION TAG	UNP P26045
A	607	HIS	-	EXPRESSION TAG	UNP P26045
A	608	HIS	-	EXPRESSION TAG	UNP P26045
A	609	HIS	-	EXPRESSION TAG	UNP P26045
A	610	HIS	-	EXPRESSION TAG	UNP P26045
A	611	SER	-	EXPRESSION TAG	UNP P26045
A	612	SER	-	EXPRESSION TAG	UNP P26045
A	613	GLY	-	EXPRESSION TAG	UNP P26045
A	614	VAL	-	EXPRESSION TAG	UNP P26045
A	615	ASP	-	EXPRESSION TAG	UNP P26045
A	616	LEU	-	EXPRESSION TAG	UNP P26045
A	617	GLY	-	EXPRESSION TAG	UNP P26045
A	618	THR	-	EXPRESSION TAG	UNP P26045
A	619	GLU	-	EXPRESSION TAG	UNP P26045
A	620	ASN	-	EXPRESSION TAG	UNP P26045
A	621	LEU	-	EXPRESSION TAG	UNP P26045
A	622	TYR	-	EXPRESSION TAG	UNP P26045
A	623	PHE	-	EXPRESSION TAG	UNP P26045
A	624	GLN	-	EXPRESSION TAG	UNP P26045
A	625	SER	-	EXPRESSION TAG	UNP P26045
A	626	ASN	-	EXPRESSION TAG	UNP P26045
A	627	ALA	-	EXPRESSION TAG	UNP P26045
A	811	ALA	ASP	ENGINEERED MUTATION	UNP P26045
A	842	SER	CYS	ENGINEERED MUTATION	UNP P26045

- Molecule 2 is a protein called Peptide from Epidermal growth factor receptor substrate 15.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	6	Total	C	H	N	O	P	5	0	0
			90	32	39	6	12	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	850	VAL	PRO	ENGINEERED MUTATION	UNP P42566

- Molecule 3 is water.

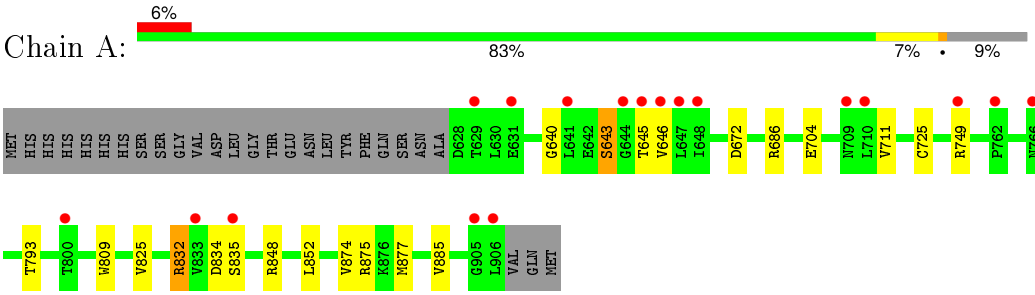
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	134	Total	O	0	0
			134	134		
3	B	3	Total	O	0	0
			3	3		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

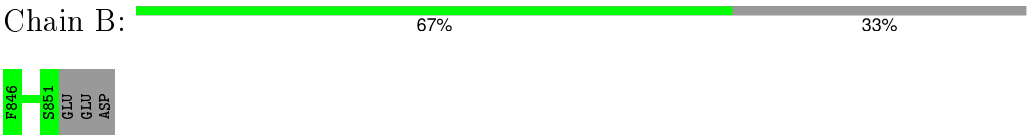
- Molecule 1: Tyrosine-protein phosphatase non-receptor type 3

Chain A:



- Molecule 2: Peptide from Epidermal growth factor receptor substrate 15

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	58.05Å 67.33Å 68.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.08 – 1.72 37.08 – 1.72	Depositor EDS
% Data completeness (in resolution range)	98.8 (37.08-1.72) 98.8 (37.08-1.72)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 1.72Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.182 , 0.229 0.184 , 0.227	Depositor DCC
R_{free} test set	1460 reflections (5.06%)	DCC
Wilson B-factor (Å^2)	19.5	Xtriage
Anisotropy	0.718	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 48.1	EDS
Estimated twinning fraction	0.023 for -h,l,k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 28864 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4707	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 6.43% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PTR

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	0.64	1/2311 (0.0%)	0.69	4/3141 (0.1%)
2	B	0.52	0/34	0.49	0/43
All	All	0.64	1/2345 (0.0%)	0.68	4/3184 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	725	CYS	CB-SG	-5.81	1.72	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	672	ASP	CB-CG-OD1	5.98	123.68	118.30
1	A	875	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	686	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	A	875	ARG	NE-CZ-NH2	-5.66	117.47	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2247	2233	2241	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	51	39	39	0	0
3	A	134	0	0	2	0
3	B	3	0	0	0	0
All	All	2435	2272	2280	12	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.

All (12) 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:832:ARG:HG2	3:A:1131:HOH:O	1.97	0.63
1:A:834:ASP:O	1:A:835:SER:OG	2.11	0.57
1:A:749:ARG:NH1	3:A:1117:HOH:O	2.41	0.54
1:A:643:SER:OG	1:A:645:THR:HG23	2.12	0.50
1:A:874:VAL:HA	1:A:877:MET:HE2	1.99	0.45
1:A:825:VAL:HG22	1:A:852:LEU:CD2	2.49	0.43
1:A:640:GLY:HA3	1:A:646:VAL:HG23	2.02	0.42
1:A:704:GLU:CG	1:A:711:VAL:HG22	2.49	0.42
1:A:825:VAL:HG22	1:A:852:LEU:HD22	2.02	0.42
1:A:809:TRP:CE2	1:A:848:ARG:HG2	2.55	0.41
1:A:771:HIS:ND1	1:A:793:THR:HG21	2.35	0.41
1:A:704:GLU:HG3	1:A:711:VAL:HG22	2.02	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	282/306 (92%)	272 (96%)	9 (3%)	1 (0%)	39 20
2	B	3/9 (33%)	3 (100%)	0	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	285/315 (90%)	275 (96%)	9 (3%)	1 (0%)	39 20

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	885	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	254/273 (93%)	249 (98%)	5 (2%)	63 43
2	B	4/7 (57%)	4 (100%)	0	100 100
All	All	258/280 (92%)	253 (98%)	5 (2%)	70 45

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	643	SER
1	A	771	HIS
1	A	788[A]	MET
1	A	788[B]	MET
1	A	832	ARG

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

Mol	Chain	Res	Type
1	A	709	ASN
1	A	771	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	PTR	B	849	2	14,16,17	1.01	1 (7%)	18,22,24	0.82	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PTR	B	849	2	-	0/9/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	849	PTR	OH-CZ	-2.99	1.33	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	849	PTR	O3P-P-OH	2.16	112.96	105.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 95^{th} 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	279/306 (91%)	0.36	18 (6%) 22 24	13, 24, 47, 56	11 (3%)
2	B	5/9 (55%)	0.31	0 100 100	21, 26, 37, 39	1 (20%)
All	All	284/315 (90%)	0.35	18 (6%) 23 25	13, 24, 46, 56	12 (4%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	905	GLY	5.6
1	A	906	LEU	4.9
1	A	648	ILE	3.2
1	A	835	SER	3.1
1	A	644	GLY	3.1
1	A	641	LEU	3.0
1	A	709	ASN	3.0
1	A	629	THR	2.9
1	A	645	THR	2.8
1	A	647	LEU	2.7
1	A	631	GLU	2.4
1	A	833	VAL	2.4
1	A	646	VAL	2.2
1	A	749	ARG	2.1
1	A	800	THR	2.1
1	A	710	LEU	2.1
1	A	766	ASN	2.1
1	A	762	PRO	2.0

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

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, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
2	PTR	B	849	16/17	0.99	0.10	-	13,17,23,26	0

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 (i)

There are no such residues in this entry.