



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:38 PM UTC

PDB ID : 1PTT / pdb_00001ptt
Title : CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B
COMPLEXED WITH PHOSPHOTYROSINE-CONTAINING TETRA-
PEPTIDE (AC-DEPYL-NH₂)
Authors : Barford, D.; Jia, Z.
Deposited on : 1995-04-21
Resolution : 2.90 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

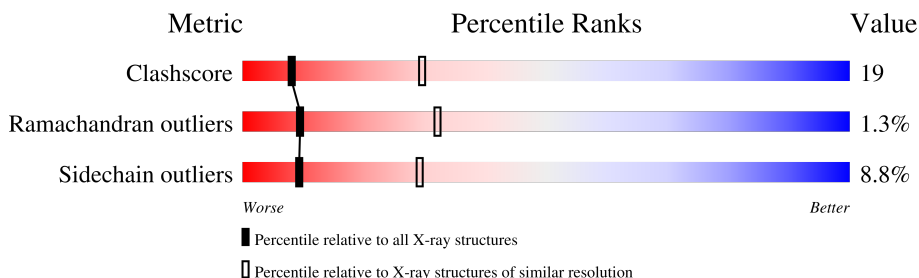
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	321	
2	B	5	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2471 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 PROTEIN TYROSINE PHOSPHATASE 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	0	0
			2427	1536	418	458	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	151	THR	SER	conflict	UNP P18031
A	215	SER	CYS	engineered mutation	UNP P18031

- Molecule 2 is a protein called PHOSPHOTYROSINE-CONTAINING TETRA-PEPTIDE.

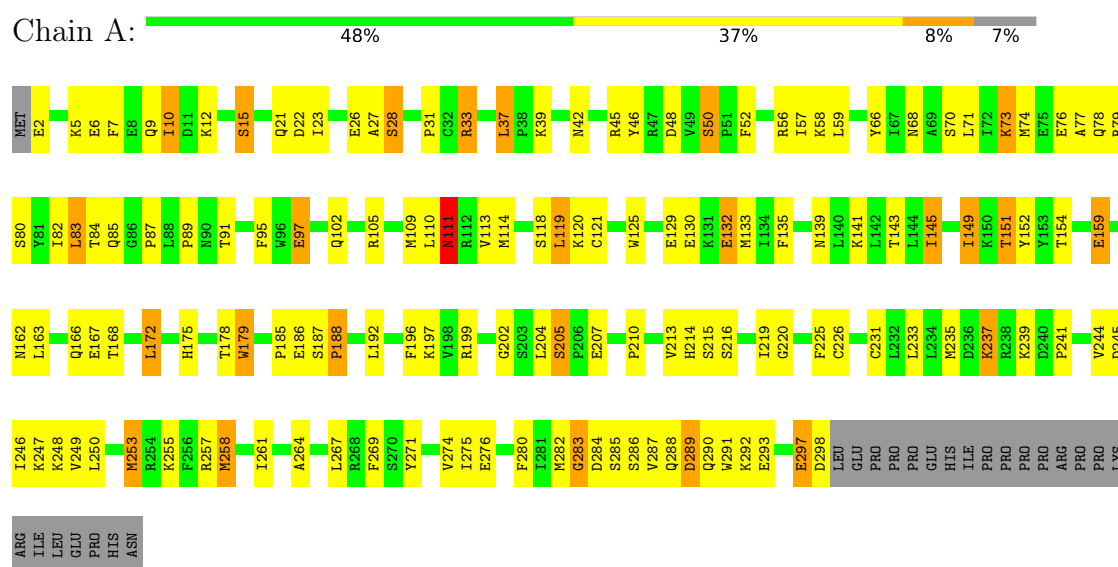
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	P	0	0	0
			44	26	4	13	1			

3 Residue-property plots

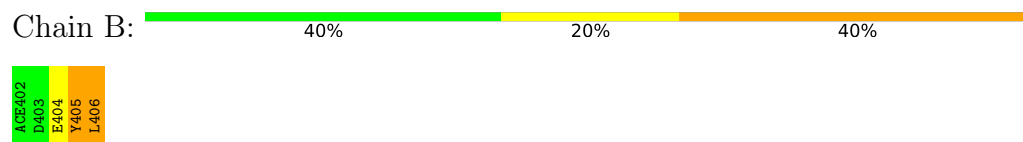
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN TYROSINE PHOSPHATASE 1B



• Molecule 2: PHOSPHOTYROSINE-CONTAINING TETRA-PEPTIDE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.50 Å 88.50 Å 124.50 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.90	Depositor
% Data completeness (in resolution range)	79.1 (6.00-2.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.194 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2471	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.20	2/2482 (0.1%)	1.34	31/3346 (0.9%)
2	B	1.17	0/24	1.88	0/30
All	All	1.20	2/2506 (0.1%)	1.35	31/3376 (0.9%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	253	MET	SD-CE	-7.04	1.61	1.79
1	A	50	SER	C-O	5.32	1.28	1.24

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	SER	N-CA-C	6.93	114.37	108.13
1	A	91	THR	N-CA-C	6.70	121.52	112.88
1	A	21	GLN	N-CA-C	-6.60	104.08	111.28
1	A	66	TYR	N-CA-C	6.32	119.95	109.46
1	A	179	TRP	CA-C-N	6.31	126.28	119.78
1	A	179	TRP	C-N-CA	6.31	126.28	119.78
1	A	244	VAL	N-CA-C	6.26	116.51	108.12
1	A	97	GLU	N-CA-C	-6.01	104.42	110.97
1	A	15	SER	N-CA-C	5.92	120.50	113.16
1	A	255	LYS	N-CA-C	-5.87	104.97	111.36
1	A	151	THR	N-CA-C	5.83	117.31	111.07
1	A	50	SER	CA-C-N	5.82	127.12	119.84
1	A	50	SER	C-N-CA	5.82	127.12	119.84
1	A	258	MET	N-CA-C	5.74	117.47	110.41
1	A	172	LEU	N-CA-C	-5.71	102.02	110.48
1	A	264	ALA	N-CA-C	-5.54	105.25	111.28
1	A	27	ALA	N-CA-C	5.53	118.25	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	197	LYS	N-CA-C	-5.46	105.02	110.97
1	A	145	ILE	N-CA-C	-5.45	107.48	111.90
1	A	26	GLU	CA-C-N	-5.39	115.28	122.72
1	A	26	GLU	C-N-CA	-5.39	115.28	122.72
1	A	111	ASN	N-CA-C	5.36	117.12	109.14
1	A	10	ILE	CB-CA-C	-5.31	105.06	112.02
1	A	22	ASP	N-CA-C	5.31	117.07	111.28
1	A	149	ILE	N-CA-C	5.22	115.73	108.84
1	A	7	PHE	N-CA-C	5.10	116.53	111.07
1	A	215	SER	N-CA-C	-5.10	99.93	110.80
1	A	52	PHE	N-CA-C	-5.08	102.53	110.10
1	A	205	SER	N-CA-C	5.05	116.25	109.83
1	A	125	TRP	CA-C-N	5.01	124.92	119.76
1	A	125	TRP	C-N-CA	5.01	124.92	119.76

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	2427	0	2383	95	0
2	B	44	0	31	3	0
All	All	2471	0	2414	95	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 19.

All (95) 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:105:ARG:HH11	1:A:105:ARG:HG3	1.44	0.82
1:A:245:ASP:HB3	1:A:248:LYS:HD2	1.63	0.79
1:A:241:PRO:HG3	1:A:282:MET:HE2	1.65	0.77
1:A:9:GLN:O	1:A:12:LYS:HG2	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:VAL:HG13	1:A:121:CYS:O	1.86	0.76
1:A:82:ILE:HG13	1:A:210:PRO:HB2	1.74	0.70
1:A:73:LYS:HE2	1:A:80:SER:OG	1.94	0.67
1:A:141:LYS:HB2	1:A:163:LEU:HD21	1.75	0.67
1:A:83:LEU:HD21	1:A:226:CYS:SG	2.37	0.65
1:A:2:GLU:O	1:A:5:LYS:HB2	1.95	0.65
1:A:87:PRO:HG3	1:A:95:PHE:CD2	2.31	0.64
1:A:57:ILE:HD11	1:A:71:LEU:HB2	1.79	0.64
1:A:70:SER:OG	1:A:257:ARG:HD2	1.98	0.64
1:A:83:LEU:HD22	1:A:213:VAL:HB	1.80	0.63
1:A:84:THR:O	1:A:214:HIS:HB2	1.98	0.62
1:A:202:GLY:O	1:A:205:SER:HB3	2.00	0.62
1:A:199:ARG:HG2	1:A:204:LEU:HD12	1.82	0.61
1:A:286:SER:O	1:A:290:GLN:HG3	2.01	0.61
1:A:283:GLY:O	1:A:285:SER:N	2.34	0.60
1:A:48:ASP:OD1	2:B:404:GLU:HA	2.01	0.60
1:A:56:ARG:HH21	1:A:58:LYS:HE2	1.67	0.60
1:A:280:PHE:CE1	1:A:288:GLN:HB2	2.38	0.58
1:A:82:ILE:CD1	1:A:102:GLN:HG3	2.34	0.57
1:A:133:MET:HE2	1:A:135:PHE:CZ	2.40	0.57
1:A:231:CYS:SG	1:A:246:ILE:HG23	2.44	0.57
1:A:119:LEU:HD22	1:A:119:LEU:N	2.18	0.57
1:A:245:ASP:CB	1:A:248:LYS:HD2	2.32	0.56
1:A:2:GLU:HB2	1:A:5:LYS:HG3	1.88	0.55
1:A:31:PRO:HB3	1:A:33:ARG:HH11	1.72	0.55
1:A:287:VAL:HA	1:A:290:GLN:CD	2.32	0.54
1:A:233:LEU:O	1:A:237:LYS:HG2	2.07	0.54
1:A:79:ARG:NH1	1:A:204:LEU:HD13	2.23	0.54
1:A:73:LYS:C	1:A:73:LYS:HD3	2.32	0.53
1:A:56:ARG:NH2	1:A:58:LYS:HE2	2.22	0.53
1:A:45:ARG:HG3	1:A:45:ARG:NH1	2.23	0.53
1:A:48:ASP:OD2	2:B:406:LEU:HB2	2.09	0.52
1:A:114:MET:HA	1:A:118:SER:O	2.10	0.52
1:A:246:ILE:HD12	1:A:271:TYR:CD1	2.45	0.52
1:A:73:LYS:HD3	1:A:74:MET:N	2.25	0.51
1:A:235:MET:HE3	1:A:274:VAL:CG1	2.41	0.51
1:A:205:SER:OG	1:A:207:GLU:HG2	2.10	0.50
1:A:23:ILE:HD12	1:A:267:LEU:HD21	1.93	0.49
1:A:6:GLU:CD	1:A:247:LYS:HZ1	2.21	0.49
1:A:292:LYS:C	1:A:292:LYS:HD3	2.37	0.49
1:A:6:GLU:OE2	1:A:247:LYS:NZ	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:LEU:O	1:A:196:PHE:HD1	1.94	0.49
1:A:82:ILE:HD11	1:A:102:GLN:HG3	1.96	0.48
1:A:149:ILE:HA	1:A:154:THR:HG23	1.94	0.48
1:A:77:ALA:HB1	1:A:233:LEU:HD23	1.95	0.48
1:A:175:HIS:CD2	1:A:175:HIS:C	2.91	0.48
1:A:280:PHE:HB2	1:A:287:VAL:CG1	2.43	0.48
1:A:132:GLU:HB3	1:A:143:THR:OG1	2.13	0.48
1:A:152:TYR:HE1	1:A:297:GLU:HB3	1.79	0.47
1:A:151:THR:OG1	1:A:297:GLU:HA	2.14	0.47
1:A:45:ARG:HG3	1:A:45:ARG:HH11	1.78	0.47
1:A:45:ARG:H	1:A:85:GLN:HE22	1.63	0.47
1:A:249:VAL:O	1:A:253:MET:HG3	2.15	0.47
1:A:10:ILE:HG23	1:A:15:SER:HB2	1.96	0.46
1:A:119:LEU:N	1:A:119:LEU:CD2	2.78	0.46
1:A:280:PHE:CZ	1:A:288:GLN:OE1	2.68	0.46
1:A:77:ALA:O	1:A:78:GLN:HB2	2.17	0.45
1:A:70:SER:OG	1:A:257:ARG:HB2	2.16	0.45
1:A:287:VAL:HG13	1:A:291:TRP:CZ2	2.52	0.45
1:A:59:LEU:HB3	1:A:97:GLU:OE2	2.16	0.45
1:A:105:ARG:HG3	1:A:105:ARG:NH1	2.18	0.45
1:A:45:ARG:HB3	1:A:85:GLN:NE2	2.32	0.45
1:A:237:LYS:HG2	1:A:237:LYS:H	1.64	0.44
1:A:105:ARG:HH11	1:A:105:ARG:CG	2.23	0.44
1:A:219:ILE:HG13	1:A:220:GLY:N	2.31	0.44
1:A:151:THR:OG1	1:A:298:ASP:N	2.51	0.44
1:A:275:ILE:O	1:A:276:GLU:C	2.61	0.43
1:A:5:LYS:O	1:A:6:GLU:C	2.61	0.43
1:A:37:LEU:HD23	1:A:39:LYS:HE2	2.01	0.43
1:A:46:TYR:CG	2:B:405:PTR:HB3	2.53	0.43
1:A:68:ASN:OD1	1:A:68:ASN:C	2.61	0.43
1:A:162:ASN:O	1:A:166:GLN:N	2.50	0.43
1:A:188:PRO:O	1:A:192:LEU:HD12	2.19	0.43
1:A:145:ILE:HD13	1:A:159:GLU:HB2	2.01	0.43
1:A:152:TYR:HB2	1:A:178:THR:OG1	2.19	0.43
1:A:105:ARG:NH1	1:A:105:ARG:CG	2.81	0.43
1:A:6:GLU:O	1:A:9:GLN:HB3	2.19	0.42
1:A:76:GLU:O	1:A:78:GLN:HG3	2.19	0.42
1:A:110:LEU:HD11	1:A:225:PHE:HB2	2.01	0.42
1:A:239:LYS:HA	1:A:239:LYS:HD2	1.85	0.42
1:A:287:VAL:HA	1:A:290:GLN:NE2	2.35	0.42
1:A:42:ASN:OD1	1:A:42:ASN:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:PRO:HB3	1:A:33:ARG:NH1	2.34	0.42
1:A:105:ARG:NH1	1:A:172:LEU:HG	2.35	0.41
1:A:185:PRO:HB2	1:A:269:PHE:CZ	2.56	0.41
1:A:120:LYS:HB3	1:A:216:SER:HB2	2.03	0.41
1:A:109:MET:HG3	1:A:111:ASN:ND2	2.34	0.41
1:A:23:ILE:HD12	1:A:267:LEU:CD2	2.51	0.41
1:A:87:PRO:CG	1:A:95:PHE:CD2	3.03	0.41
1:A:289:ASP:O	1:A:293:GLU:HG2	2.21	0.40
1:A:110:LEU:HD13	1:A:179:TRP:CZ3	2.56	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	295/321 (92%)	272 (92%)	19 (6%)	4 (1%)	9	30
2	B	2/5 (40%)	1 (50%)	1 (50%)	0	100	100
All	All	297/326 (91%)	273 (92%)	20 (7%)	4 (1%)	9	32

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	ASP
1	A	28	SER
1	A	261	ILE
1	A	283	GLY

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	270/294 (92%)	247 (92%)	23 (8%)	10	31
2	B	3/3 (100%)	2 (67%)	1 (33%)	0	0
All	All	273/297 (92%)	249 (91%)	24 (9%)	9	29

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	33	ARG
1	A	37	LEU
1	A	50	SER
1	A	73	LYS
1	A	83	LEU
1	A	89	PRO
1	A	111	ASN
1	A	119	LEU
1	A	129	GLU
1	A	130	GLU
1	A	132	GLU
1	A	139	ASN
1	A	159	GLU
1	A	167	GLU
1	A	168	THR
1	A	186	GLU
1	A	188	PRO
1	A	237	LYS
1	A	250	LEU
1	A	258	MET
1	A	289	ASP
1	A	297	GLU
2	B	406	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	61	GLN
1	A	85	GLN
1	A	111	ASN
1	A	123	GLN
1	A	166	GLN
1	A	290	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	405	2	15,16,17	1.08	1 (6%)	17,22,24	2.27	5 (29%)

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	405	2	-	0/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	405	PTR	CE2-CD2	2.53	1.42	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	405	PTR	O3P-P-OH	5.55	121.74	105.32
2	B	405	PTR	OH-P-O1P	5.05	126.32	109.48
2	B	405	PTR	O2P-P-O1P	-3.58	96.87	110.83
2	B	405	PTR	O3P-P-O1P	-2.52	101.01	110.83
2	B	405	PTR	P-OH-CZ	2.01	131.05	123.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	405	PTR	1	0

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.