



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:18 PM GMT

PDB ID : 1A55
Title : PHOSPHATE-BINDING PROTEIN MUTANT A197C
Authors : Hirshberg, M.; Henrick, K.; Lloyd-Haire, L.; Vasisht, N.; Brune, M.; Corrie, J.E.T.; Webb, M.R.
Deposited on : 1998-02-19
Resolution : 2.40 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

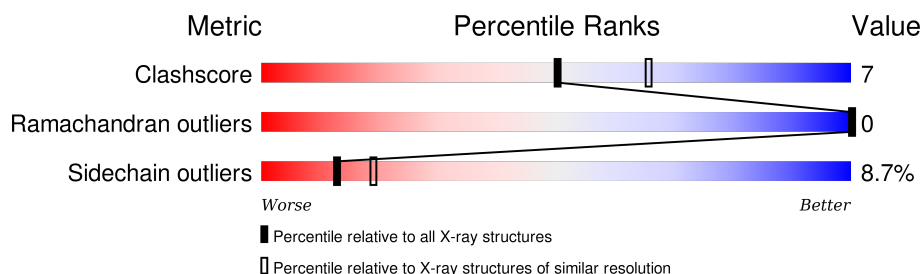
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)

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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	321	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2717 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.

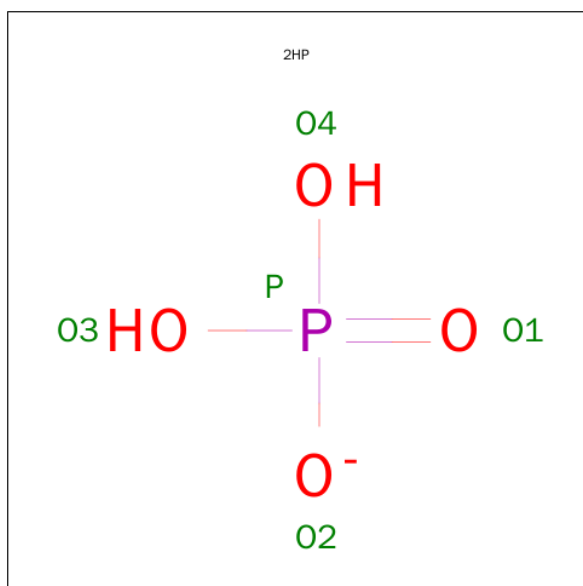
- Molecule 1 is a protein called PHOSPHATE-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	321	2444	1559	406	478	1	0	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	CYS	ALA	ENGINEERED	UNP P06128

- Molecule 2 is DIHYDROGENPHOSPHATE ION (three-letter code: 2HP) (formula: $\text{H}_2\text{O}_4\text{P}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0

- Molecule 3 is water.

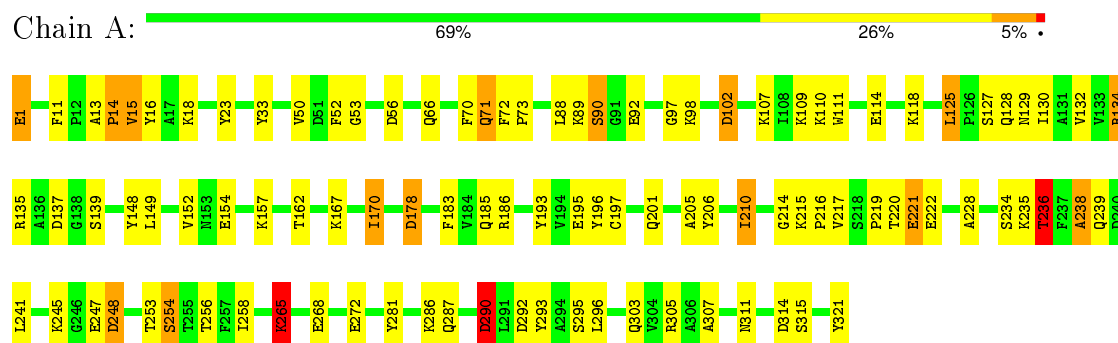
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	268	Total 268	O 268	0	0

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.

Note EDS was not executed.

• Molecule 1: PHOSPHATE-BINDING PROTEIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	42.04 Å 64.16 Å 124.35 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.40	Depositor
% Data completeness (in resolution range)	86.6 (12.00-2.40)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.173 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2717	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: 2HP

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	2/2508 (0.1%)	1.86	68/3402 (2.0%)

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	A	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	195	GLU	CD-OE1	-6.27	1.18	1.25
1	A	53	GLY	N-CA	5.01	1.53	1.46

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	GLU	CA-CB-CG	9.89	135.17	113.40
1	A	134	ARG	NE-CZ-NH1	9.11	124.86	120.30
1	A	193	TYR	CB-CG-CD2	-9.00	115.60	121.00
1	A	221	GLU	OE1-CD-OE2	-8.09	113.59	123.30
1	A	314	ASP	CB-CG-OD1	7.99	125.49	118.30
1	A	102	ASP	CB-CG-OD1	7.93	125.43	118.30
1	A	290	ASP	CA-C-O	-7.85	103.62	120.10
1	A	314	ASP	CB-CG-OD2	-7.62	111.44	118.30
1	A	162	THR	CA-CB-CG2	7.46	122.84	112.40
1	A	272	GLU	CG-CD-OE1	7.24	132.77	118.30
1	A	281	TYR	CB-CG-CD2	-7.22	116.67	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	52	PHE	CB-CG-CD1	7.21	125.85	120.80
1	A	135	ARG	NE-CZ-NH2	7.19	123.90	120.30
1	A	321	TYR	CB-CG-CD1	7.13	125.28	121.00
1	A	292	ASP	CB-CG-OD2	-7.12	111.89	118.30
1	A	305	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	A	72	PHE	CB-CG-CD2	7.07	125.75	120.80
1	A	72	PHE	CG-CD2-CE2	7.05	128.55	120.80
1	A	220	THR	CA-CB-CG2	6.98	122.17	112.40
1	A	293	TYR	CB-CG-CD2	6.90	125.14	121.00
1	A	149	LEU	CB-CG-CD1	-6.83	99.39	111.00
1	A	148	TYR	CB-CG-CD2	-6.72	116.97	121.00
1	A	137	ASP	CB-CG-OD1	6.67	124.30	118.30
1	A	281	TYR	CB-CG-CD1	6.64	124.98	121.00
1	A	290	ASP	CA-C-N	6.57	131.66	117.20
1	A	193	TYR	CB-CG-CD1	6.57	124.94	121.00
1	A	154	GLU	CG-CD-OE2	-6.51	105.28	118.30
1	A	154	GLU	CG-CD-OE1	6.48	131.25	118.30
1	A	33	TYR	CB-CG-CD2	-6.46	117.13	121.00
1	A	196	TYR	CB-CG-CD1	-6.39	117.17	121.00
1	A	139	SER	C-N-CA	6.33	135.60	122.30
1	A	15	VAL	CB-CA-C	-6.30	99.43	111.40
1	A	1	GLU	CG-CD-OE2	-6.22	105.86	118.30
1	A	114	GLU	CG-CD-OE1	6.20	130.71	118.30
1	A	52	PHE	CB-CG-CD2	-6.17	116.48	120.80
1	A	292	ASP	OD1-CG-OD2	6.16	134.99	123.30
1	A	272	GLU	N-CA-CB	-6.15	99.53	110.60
1	A	71	GLN	CA-CB-CG	6.02	126.64	113.40
1	A	1	GLU	CG-CD-OE1	5.85	130.00	118.30
1	A	221	GLU	CG-CD-OE1	5.83	129.96	118.30
1	A	11	PHE	CZ-CE2-CD2	-5.81	113.12	120.10
1	A	292	ASP	CB-CG-OD1	-5.76	113.11	118.30
1	A	114	GLU	OE1-CD-OE2	-5.69	116.47	123.30
1	A	296	LEU	O-C-N	5.64	131.82	121.10
1	A	125	LEU	CA-CB-CG	5.63	128.25	115.30
1	A	307	ALA	CB-CA-C	5.58	118.48	110.10
1	A	196	TYR	CB-CG-CD2	5.45	124.27	121.00
1	A	222	GLU	OE1-CD-OE2	-5.44	116.77	123.30
1	A	290	ASP	CB-CG-OD1	5.38	123.14	118.30
1	A	321	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	A	170	ILE	CA-CB-CG2	5.34	121.59	110.90
1	A	16	TYR	CB-CG-CD2	-5.28	117.83	121.00
1	A	206	TYR	O-C-N	5.27	131.14	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	GLU	CA-CB-CG	5.23	124.91	113.40
1	A	14	PRO	O-C-N	-5.23	114.33	122.70
1	A	66	GLN	N-CA-CB	5.22	120.00	110.60
1	A	254	SER	O-C-N	5.21	131.04	122.70
1	A	248	ASP	CB-CG-OD1	5.20	122.98	118.30
1	A	23	TYR	CA-CB-CG	5.19	123.27	113.40
1	A	15	VAL	CA-CB-CG2	5.09	118.54	110.90
1	A	219	PRO	C-N-CA	5.07	134.38	121.70
1	A	272	GLU	OE1-CD-OE2	-5.07	117.21	123.30
1	A	265	LYS	CA-CB-CG	5.05	124.52	113.40
1	A	222	GLU	C-N-CA	5.04	134.30	121.70
1	A	239	GLN	O-C-N	5.04	130.76	122.70
1	A	70	PHE	CB-CA-C	5.04	120.47	110.40
1	A	293	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	A	135	ARG	NH1-CZ-NH2	-5.03	113.87	119.40

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	178	ASP	Mainchain
1	A	236	THR	Mainchain
1	A	238	ALA	Mainchain
1	A	265	LYS	Mainchain
1	A	290	ASP	Mainchain
1	A	311	ASN	Mainchain
1	A	50	VAL	Mainchain

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	2444	0	2416	34	1
2	A	5	0	0	0	0
3	A	268	0	0	12	3
All	All	2717	0	2416	34	3

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 7.

All (34) 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:234:SER:HA	1:A:303:GLN:HE22	1.38	0.88
1:A:236:THR:HG22	1:A:238:ALA:H	1.56	0.71
1:A:248:ASP:OD2	3:A:840:HOH:O	2.11	0.66
1:A:18:LYS:CD	1:A:287:GLN:HE21	2.16	0.59
1:A:217:VAL:HG11	1:A:248:ASP:HA	1.84	0.58
1:A:235:LYS:NZ	3:A:616:HOH:O	2.36	0.58
1:A:286:LYS:HB3	3:A:434:HOH:O	2.06	0.56
1:A:210:ILE:HD12	1:A:214:GLY:HA2	1.88	0.55
1:A:18:LYS:HD3	1:A:287:GLN:HE21	1.73	0.53
1:A:197:CYS:SG	1:A:201:GLN:NE2	2.82	0.53
1:A:89:LYS:HB3	3:A:821:HOH:O	2.09	0.51
1:A:247:GLU:HG2	3:A:529:HOH:O	2.10	0.51
1:A:107:LYS:NZ	3:A:457:HOH:O	2.41	0.51
1:A:210:ILE:CD1	1:A:214:GLY:HA2	2.41	0.50
1:A:107:LYS:HA	3:A:531:HOH:O	2.12	0.50
1:A:1:GLU:N	3:A:665:HOH:O	2.41	0.47
1:A:185:GLN:NE2	3:A:522:HOH:O	2.43	0.46
1:A:97:GLY:HA3	1:A:152:VAL:HG21	1.98	0.45
1:A:111:TRP:CE2	1:A:130:ILE:HG12	2.51	0.45
1:A:110:LYS:NZ	1:A:129:ASN:OD1	2.38	0.45
1:A:102:ASP:O	1:A:107:LYS:HB2	2.16	0.45
1:A:73:PRO:HA	1:A:256:THR:O	2.17	0.45
1:A:90:SER:OG	1:A:205:ALA:HA	2.16	0.45
1:A:88:LEU:HB3	3:A:663:HOH:O	2.16	0.45
1:A:18:LYS:HD3	1:A:287:GLN:NE2	2.31	0.45
1:A:134:ARG:HD2	1:A:134:ARG:C	2.38	0.45
1:A:13:ALA:HB3	1:A:14:PRO:HD3	1.99	0.44
1:A:71:GLN:HA	1:A:258:ILE:O	2.18	0.44
1:A:228:ALA:HA	1:A:241:LEU:HD22	2.00	0.43
1:A:132:VAL:HB	1:A:170:ILE:HD12	2.01	0.42
1:A:286:LYS:HG2	3:A:686:HOH:O	2.19	0.42
1:A:185:GLN:HG3	3:A:817:HOH:O	2.19	0.42
1:A:253:THR:HG22	1:A:254:SER:N	2.36	0.41
1:A:215:LYS:HA	1:A:216:PRO:HD3	1.79	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:ASP:O	3:A:838:HOH:O[3_655]	1.60	0.60
3:A:423:HOH:O	3:A:624:HOH:O[3_645]	1.66	0.54
3:A:721:HOH:O	3:A:755:HOH:O[4_455]	1.98	0.22

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	321/321 (100%)	309 (96%)	12 (4%)	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	254/253 (100%)	232 (91%)	22 (9%)	13	19

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	56	ASP
1	A	90	SER
1	A	98	LYS
1	A	109	LYS
1	A	118	LYS

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Mol	Chain	Res	Type
1	A	125	LEU
1	A	127	SER
1	A	128	GLN
1	A	157	LYS
1	A	167	LYS
1	A	178	ASP
1	A	183	PHE
1	A	186	ARG
1	A	210	ILE
1	A	221	GLU
1	A	236	THR
1	A	245	LYS
1	A	265	LYS
1	A	268	GLU
1	A	295	SER
1	A	315	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	201	GLN
1	A	287	GLN
1	A	303	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

1 ligand 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	2HP	A	322	1	4,4,4	1.66	1 (25%)	6,6,6	1.92	2 (33%)

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	2HP	A	322	1	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	322	2HP	P-O3	-2.62	1.45	1.55

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	322	2HP	O4-P-O2	-2.92	100.91	109.06
2	A	322	2HP	O3-P-O2	3.42	118.60	109.06

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.